

FIGURE 2

MLAARLVCLRTLPSRVFHPAFTKASPVVKNSITKNQWLLTPSREYATKTRIGIRRGRGTQDEL
KEAALEPSMEKIFKIDQMGRWVFVAGGAAVGLGALCYYGGLSNEIGAIEKAVIWPQYVKDRI
HSTYMYLAGSIGLTALSAIAISRTPVLMNFMMRGSWVTIGVTFAAMVGAGMLVRSIPYDQSP
GPKHLAWLLHSGVMGAVVAPLTILGGPELLIRAAWYTAGIVGGLSTVAMCAPSEKFLNMGAPL
GVGLGLVVFVSSLGSMFLPPTTVAGATLYSVAMYGGGLVLFMFLLYDTQKVIKRAEVSPMYGV
QKYDPINSMLSIIYMDTLNIFMRVATMLATGGNRKK

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FIGURE 3

GAAGGCTGCCTCGCTGGTCCGAATTCGGTGGCGCCACGTCGCCCGCTCTCCGCCCTCTGCAT
 CGCGGCTTCGGCGGCTTCCACCTAGACACCTAACAGTCGCGGAGCGCGCGCTCGTGAGGG
 GTTCGGCAGCGGGAGTCGGGCGGTCTGTGCATCTTGGCTACCTTGGGTGCGAAGATGTCGG
 ACATCGGAGACTGGTTCAGGAGCATCCCGCGCATCACGCGCTATTGGTTTCGGCGCCACCGTC
 GCGGTGCCCTTGGTCGGCAAACTCGGCCCTCATCGCCGCGCTACCTCTTCCCTCGCCCGGA
 AGCCTTCCTTTATCGCTTTCAGATTGGAGGCCAATCACTGCCACCTTTTATTTCCCTGTGG
 GICCAGGAAGTCGGATTTCTTTATTTGGTCAATTTATATTTCTATATCAGTATTTCTACGCA
 CTTGAAACAGGAGCTTTTGATGGGAGGCCAGCAGACTATTTATTCATGCTCCTCTTTAACTG
 GATTTCATCGTGATTACTGGCTTAGCAATGGATATGCAGTTGCTGATGATTCCTCTGATCA
 TGTCACTACTTTATGCTCGGGCCAGCTGAACAGAGACATGATTGATCATTTTGGTTTGGGA
 ACACGATTTAAGGCTGCTATTACCTGGGTTATCCTTGGATTCAACTATATCATCGGAGG
 CTCGGTAATCAATGAGCTTATTGGAATCTGGTTGGACATCTTTATTTTTCTTAATGTTCA
 GATACCCAATGGACTTGGGAGGAAGAAATTTCTATCCACACCTCAGTTTTTGTACCGCTGG
 CTGCCCCAGTAGGAGAGGAGGATATCAGGATTTGGTGTGCCCCCTGCTAGCATGAGCGGAG
 TGCTGATCAGAATGGCGGAGCGGGAGACACAACCTGGGGCCAGGGCTTCGACTTGGAGACC
 AGTGAAGGGGCGGCTCGGGCAGCCGCTCCTCTCAAGCCACATTTCTCCAGTGCTGGGTG
 CACTTAACAACCTGCGTTCTGGCTAACACTGTTGGACCTGACCCACACTGAATGTAGTCTTTC
 AGTACGAGACAAAGTTTCTTAAATCCCGAAGAAAAATATAAGTGTGTTCCAAAGTTTACAGAT
 TCTCATTTCAAGTCTTACTGCTGTGAAGAACAATAACCACTGTGCAAAATGCAAAACTGAC
 TACATTTTGGTGTCTCTCTCTCTCCCCCTTCGCTGTAATTAATGGGTTTTCAGCGGTCCT
 AATCTGCTGGCATTTGAGCTGGGCTGGGTCAACAAACCTTCCCAAAGGACCTTATCTCTT
 TCTTGCACACATGCTCTCTCCCACTTTTCCCAACCCCCACATTTGCAACTAGAAAAAGTTG
 CCGATAAAATTTGCTCGCCCTTGACAGGTTCTGTTATTTATTGACTTTTGCCAAAGGCTGGT
 ACAACAATCATATTACGTTATTTTCCCTTTTGGTGGCAGAACTGTACCAATAGGGGGGAG
 AAGACAGCCACGGATGAAGCGTTTTCTCAGCTTTTGGAAATGCTTCGACTGACATCCGTTGTT
 AACCGTTTGGCACTTTCAGATATTTTTTATAAAAAAGTACCACGTGAGTTTCATGAGGGCCA
 CAGATTTGGTTATTAATGAGATACGAGGTTGGTGTGCTGGGTGTTTGTTCCTGAGCTAAGTGA
 TCAAGACTGTAGTGGAGTTGCAGCTAACATGGGTAGGTTTAAACCATGGGGGATGCACCCG
 TTTGCGTTTCATATTAGCCCTACTGGCTTTGTGAGCTGGAGAGTGGGTTGCTTTGTGT
 TAGGAGGATCCAGATCATGTGGCTACAGGGAGATGCTCTCTTTGAGAGGTCCTGGGCAATG
 ATTCCCATTTCAATCTATTCTGGATATGTGTTCAATTGAGTAAAGGAGGAGAGACCCCAATA
 CGCTATTTAAATGTCACTTTTGGCTATCCCCCGTTTTTGGTCTAGTGTTCATTAATTTGT
 GAGGAAGGCGCAGCTCTCTGCACGTAGATCATTTTTTAAAGCTTAATGTAAGCACATCTA
 AGGGAATAAATCATGATTTAAGGTTGAATGGCTTTAGAATCATTTGGGTTTGGAGGTTGTTA
 TTTTGAGTCAATGAATGTACAAGCTCTGTAATCAGACAGCTTAAATACCCACGCTTTTTT
 TCGTAGTGGGCTTTTCCATATCAGAGCTTGGCTCATAAACCAATAAAGTTTTTTGAAGGCCA
 TGGCTTTTACACAGTTATTTTTTATGAGCTTATCTGAAAGCAGACTGTTTAGGAGCAGT
 ATTGAGTGGCTGTCACTTTTGAAGCACTAAAAAGGCTTCAACGTTTTGATCAGTTTCTT
 TCTCAGGAACATTGTGCTCTAACAGTATGACTATTTCTTCCCCACTTTAAACAGTGTGAT
 GTGTGTTATCCTAGGAAATGAGAGTTGGCAACAACTTCTCATTTTGAATAGAGTTTGTGTG
 TACTTCTCCATATTTAATTTATATGATAAAATAGGTGGGAGAGCTGGAACCTTTAACTGTCA
 TGTTTTGTGTTCATCTGTGGCCACAATAAGTTTACTTGTAAAAATTTAGAGGCCATTTACT
 CCAATTTATGTGCAGCTACACTATTGTACAGGCGTGGAGACTCATGTGATGTATAAGAAAT
 TTTCTGACAGTGAGTGACCCGAGTCTCTGGTGTACCCCTCTTACCACTGAGCTGCCGCGAG
 CAGTCAATTTTTTCTTAAAGGTTTACAAGTATTTAGAATTTTTTTCAGTTCAGGGCAAAAGTTC
 ATGAAGTTTATTTCTTAAACATGGTTAGGAAGCTGATGAGTTTATGATTTTGTCTGGATT
 ATGTTTCTGGAATAATTTTACCAAAACAAGCTATTTGAGTTTTGACTTGACAGGCAAAACA
 TGACAGTGGATTCTCTTTACAAATGAAAAAATAATCCTTATTTGTATAAAGGACTTCCC
 TTTTGTAACTAATCCTTTTATTGGTAAAAATGTAAATTAAGTGTCAACTTG

FIGURE 4

MSDIGDWFRSIPAITRYWFAATVAVPLVGKLGGLISPAYLFLWPEAFLYRFQIWRPITATFYF
PVGPGTGFLYLVLNLYFLYQYSTRLETGAFDGRPADYLFMLLFNWICIVITGLAMDMQLLMIP
LIMSVLYVWAQLNRDMIVSFWFGTRFKACYLPWVILGFNYIIGGSVINELIGNLVGHLYFFL
MFRYPMDLGGRNFLSTPQFLYRWLPSSRRGGVSGFGVPPASMRRAADQNGGGGRHNWGQGFRL
GDQ

Transmembrane domain:

amino acids 98-116, 152-172

N-myristoylation site.

amino acids 89-95, 168-174, 176-182, 215-221, 221-227, 237-243

Glycosaminoglycan attachment site.

amino acids 218-222

FIGURE 5

GGGGCCGCGGTCTAGGGCGGCTACGTGTGTTGCCATAGCGACCATTTTGCATTAACTGGTTG
 GTAGCTTCTATCCTGGGGGCTGAGCGACTGCGGGCCAGCTCTTCCCCTACTCCCTCTCGGCT
 CCTTGTGGCCCAAAGGCCTAACCGGGGTCCGGCGGTCTGGCCTAGGGATCTTCCCCGTGGC
 CCTTTGGGGCGGG**ATG**GGCTGCGGAAGAAGAAGACGAGGTGGAGTGGGTAGTGGAGAGCATCG
 CGGGGTTCCTGCGAGGCCAGACTGGTCCATCCCCATCTTGGACTTTGTGGAACAGAAATGT
 GAAGTTAACTGCAAAGGAGGGCATGTGATAACTCCAGGAAGCCCAGAGCCGGTGATTTTGGT
 GGCTGTGTTCCCTTGTTTTTGATGATGAAGAAGAAAGCAAATTGACCTATACAGAGATTC
 ATCAGGAATACAAAGAACTAGTTGAAAAGCTGTTAGAAGGTTACCTCAAAGAAATTGGAATT
 AATGAAGATCAATTTCAAGAAGCATGCACTTCTCCTCTTGCAAAGACCCATACATCACAGGC
 CATTTTGCAACCTGTGTTGGCAGCAGAAGATTTTACTATCTTTAAAGCAATGATGGTCCAGA
 AAAACATTGAATGCAGCTGCAAGCCATTTCGAATAATTCAAGAGAGAAATGGTGTATTACCT
 GACTGCTTAACCGATGGCTCTGATGTGGTCAGTGACCTTGAACACGAAGAGATGAAAATCCT
 GAGGGAAGTTCTTAGAAAATCAAAGAGGAATATGACCAGGAAGAAGAAAGGAAGAGGAAAA
 AACAGTTATCAGAGGCTAAAACAGAAGAGCCACAGTGCATTCCAGTGAAGCTGCAATAATG
 AATAATTCCCAGGGGATGGTGAACATTTTGACACCCACCCCTCAGAAGTTAAAATGCATTT
 TGCTAATCAGTCAATAGAACCCTTGGGAAGAAAAGTGGAAAGGTCTGAAACTTCCTCCCTCC
 CACAAAAAGGCCTGAAGATTCTTGGCTTAGAGCATGCGAGCATGAAGGACCAATAGCAAAC
 TTATCAGTACTTGGAACAGAAGAACTTCGGCAACGAGAACTATCTCAAGCAGAAGAGAGA
 TAAGTTGATGTCCATGAGAAAGGATATGAGGACTAAACAGATACAAAATATGGAGCAGAAAG
 GAAAACCCACTGGGAGGTAGAGGAAATGACAGAGAAACCAGAAATGACAGCAGAGGAGAAAG
 CAAACATTACTAAAGAGGAGATTGCTTGCGAGAGAACTCAAAGAAGAAGTTATTAATAAG**TA**
ATAATTAAGAACAATTTAACAAATGGAAGTTCAAATTGTCTTAAAAATAAATTATTTAGTC
 CTTACACTG

FIGURE 6

MAAEEDEVEWVVESIAGFLRGPDWSIPILDFVEQKCEVNCCKGGHVITPGSPPEPVILVACVP
LVFDDEEESKLTYTEIHQYKELVEKLLEGYLKEIGINEDQFQEACTSPLAKHTTSQAILQP
VLAAEDFTIFKAMMVQKNIEMLQAIIRIIQERNGVLPDCLTDGSDVVSdleHEEMKILREVL
RKSKEEYDQEEERKRKKQLSEAKTEEPTVHSSEAAIMNNSQGDGEHFAHPPSEVKMHFANQS
IEPLGRKVERSETSSLPQKGLKIPGLEHASIEGPIANLSVLGTEELRQREHYLKQKRDKLMS
MRKDMRTKQIQNMEQKGKPTGEVEEMTEKPEMTAEKQTLKRRLLAEKLKEEVINK

N-glycosylation sites.

amino acids 224-228, 246-250, 285-289

N-myristoylation site.

amino acids 273-279

Amidation site.

amino acids 252-256

Cytosolic fatty-acid binding proteins.

amino acids 78-108

FIGURE 7

GGGCACAGCACATGTGAAGTTTTTGATGATGAAGAAGAAAGCAAATTGACCTATACAGAGAT
TCATCAGGAATACAAAGAACTAGTTGAAAAGCTGTTAGAAGGTTACCTCAAAGAAATTGGAA
TTAATGAAGATCAATTTCAAGAAGCATGCACCTTCTCCTCTTGCAAAGACCCATACATCACAG
GCCATTTTTGCAACCTGTGTTGGCAGCAGAAGATTTTACTATCTTTAAGCAATGATGGTCC
AGAAAAACATTGAAATGCAGCTGCAAGCCATTCGAATAATTCAAGAGAGAAATGGTGTATTA
CCTGACTGCTTAACCGATGGCTCTGATGTGGTCAGTGACCTTGAACACGAAGAGATGAAAT
CCTGAGGGAAGTTCTTAGAAAATCAAAGAGGAATATGACCAGGAA

FIGURE 8

GCGTGGTTTTTGTCTGCAATAGCGGCTTAGAGGGAGGGGCTTTTTGCGCTATACCTACTG
 TAGCTTCTCCACGTATGGACCCATAAGGCTACTGCTGCTACTACGGGGTAGACAGTTACTG
 TCTCAGCTCTAGGATGTGCGTTCTTCCACTAGAAGCTCTTCTGAGGGAGGTAATAAAAAC
 AGTGGGAATGGAAGAAAAACAGTGCCTGTAGTCACTCCTGTAATATGCTCCTTGTCAACAATGTATAC
 ATTCTCTCTAGGTGCCATATTCTTCTTAAAGCTCAAGTCGCATCTTACTAGTGAAGTATT
 CTGCCAATGAAGAAAAACAAGTATGATTATCTTCCAACCTACTGTGAATGTGTGCTCAGAACCTG
 GTGAAGCTAGTTTTCTGTGTGCTTGTGTCATTCTGTGTTATAAAGAAAGATCATCAAAGTAG
 AAATTTGAAATATGCTTCTTGAAGGAATCTCTGATTTCATGAAGTGGTCCATTCTCGCT
 TTCTTTATTTCTGGATAAATTGATTGTCTTCTATGTCCTGTCTTATCTTCAACAGCCATG
 GCTGTTATCTTCTCAAATTTAGCATTATAACAACAGCTCTTCTATTTCAGGATAGTGCTGAA
 GAGGCGTCTAAACTGGATCCAGTGGGCTTCCCTCTGACTTTATTTTTGTCTATTGTGGCCT
 TGACTGCCGGGACTAAAACTTTACAGCACAACTTGGCAGGACGTGGATTTCATCCAGATGCC
 TTTTTCAGCCCTTCCAATTCCTGCCCTTCTTTTTCAGAAGTGAGTGTCCAGAAAAGACAATTG
 TCAGACGAAGAAGATGGACTTTTCTGAGCTAAATGGAACACCACAGCCAGAGTTTTCAGTC
 ACATCCGCTCTTGGCATGGGCCATGTTCTTATATAGTCCAGTGTTTTATTCTTCAATGGCT
 AATATCTATAATGAAAGATACTGAAGGAGGGGAACAGCTCACTGAAAGCATCTTCATACA
 GAACAGCAAACTCTATTCTTTTGGCATTCTGTTTTAATGGGCTGACTCTGGGCCCTTCAGAGGA
 GTAACCGTGATCAGATTAAAGACTGTGGATTTTTTATGGCCACAGTGCAATTTTCAGTACCC
 CTATATTTTGAATGCAATTCAGGGGCTTTTCAGTGGCTTTCATTCTGAAGTTCCTGGATAA
 CATGTTCCATGTCTTGTATGGCCAGGTACCACGTGCATTATCACAAACAGTGTCTGTCTGG
 TCTTTGACTTCAGGCCCTCCCTGGAATTTTTCTTGGAAAGCCCCATCAGTCCCTCTCTATA
 TTTATTTATAATGCCAGCAAGCTCAAGTTCGGGAATACGCACCTAGGCAAGAAAGGATCCG
 AGATCTAAGTGGCAATCTTTTGGAGCGTTCCAGTGGGGATGGAGAAGACTAGAAAGACTTA
 CCAACCCAAAGATGATGAGTCAGATGAAGATACTTTCTAAGTGGTACCCACATAGTTTGC
 GCTCTCTTGAACCTTATTTTTCACATTTTCAGTGTTTGAATATTTATCTTTTCACTTTGATA
 AACCAGAAATGTTTCTAAATCCTAATATCTTGTGATATATCTAGCTACTCCCTAAATGGT
 CCATCCAAGGCTTAGAGTACCCAAAGGCTAAGAAATCTAAGAACTGATACAGGAGTAACA
 ATATGAAGAATTCATTAATATCTCAGTACTTGATAAATCAGAAAGTTATATGTGCAGATTAT
 TTTCTTGGCCTTCAAGCTTCCAAAAAATCTGTAATATCATGTTAGCTATAGCTTGTATAT
 ACACATAGAGATCAATTTGCCAAATATTCACAATCATGTAGTCTTACATGCTTACATGCCAAAGT
 CTCCCTTTTAAACATATAAAAAGCTAGGTTGTCTCTTGAATTTTGGAGGCCCTAGAGATAGT
 CATTTTGTGAAGTAAAGAGCAACGGGACCCCTTCTAAAAACGTTGGTTGAAGGACCTAAATAC
 CTGGCCATACCATAGTTTGGGATGATGTAGTCTGTGCTAAATATTTTGTCTGAAGAAGCAGT
 TTCTCAGACACAACATCTCAGAATTTTAATTTTGAAGAAATCATGGGAAATTGGATTTTGT
 AATAATCTTTTGTATGTTTTAAACATTTGGTTCCTTAGTCACCATAGTTACCACTTGTATTTA
 AGTCATTTAAACAAGCCACGTTGGGGCTTTTTCTCCTCAGTTTGAAGGAGAAAATCTTGAT
 GTCATTACTCTGAATTTATACATTTTGGAGAAATAGAGGGCATTTTTTATTATAGTTACT
 AATTCAAGCTGTGACTATTGTATATCTTTCCAAGAGTTGAATGCTGGCTTCAGAACTATAC
 CAGATTGTCAAGTGAAGCTGATGCCATAGGAACCTTTAAAGGGATCCTTTCAAAGGATCACT
 AGCAACACATGTTGACTTTTAACTGATGATGAATATTAATACTCTAAAAATAGAAAGACC
 AGTAATATATAAGCTCTTTACAGTGCCTTACACTTAAAGTGCATGGTATTTTTCATG
 GTATTTTGCATGCAGCCAGTTAACTCTCGTAGATAGAGAAGTCAGGTGATAGATGATATTA
 AAATTTAGCAAAACAAAAGTGACTTGTCTCAGGGTCACTGAGCTGGGTGATGATAGAAGAGTGGG
 CTTTAACTGGCAGGCTGTATGTTTACAGACTACCATACTGTAATAATGAGCTTTATGGTGT
 CATCTTCAGAAACTTATACATTTCTGCTCTCCTTTCTCCTAAGTTTCATGCAGATGAATATA
 AGGTAATATACTATTATAAATTTCAATTTGTGATATCCACAATAATATGACTGGCAAGTATG
 GTGGAATAATTTGTAATTAATAATTTTAAACCT

FIGURE 9

MEKQCCSHPVICSLSTMVTFLLGAIFIALSSSRILLVKYSANEENKYDYLPTTVNVCSELVK
LVFCVLVSFCVIKKDHQSRNLKYASWKEFSDFMKWSIPAFLYFLDNLIVFYVLSYLPAMAV
IFSNFIIITALLFRIVLKRRLNWIQWASLLTLFLSIVALTAGTKTLQHNLAGRGFHHDAFF
SPSNSCLLFRSECPKRDNCTAKEWTFPEAKWNTTARVFSHIRLGMGHVLIIVQCFISSMANI
YNEKILKEGNQLTESIFIQNSKLYFFGILFNGLTLGLQRSNRDQIKNCGFFYGHSAFSVALI
FVTAFAQGLSVAFILKFLDNMFHVLMAQVTTVIITTVSVLVFDFRPSLEFFLEAPSVLISIFI
YNASKPQVPEYAPRQERIRDLSGNLWERSSSGDGEELERLTKPKSDESEDTF

Transmembrane domains:

amino acids 16-36 (type II), 50-74, 147-168, 229-250, 271-293,
298-318, 328-368

N-glycosylation sites.

amino acids 128-132, 204-208, 218-222, 374-378

Glycosaminoglycan attachment site.

amino acids 402-406

N-myristoylation sites.

amino acids 257-263, 275-281, 280-286, 284-290, 317-323

FIGURE 10

CGTGCCTGCGCAATGGGTGTCGGGTCCGCTTTTCCCAATCCGGACGTAATCGTGGTTTTTG
TTCTGCAATAGGCGGCTTAGAGGGAGGGGCTTTTTCGCTATACCTACTGTAGCTTCTCCAC
GTATGGACCCCTAAAGGCTACTGCTGCTACTACGGGGCTAGACAGTTACTGTCTCAGCTCTAG
GATGTGCGTTCTTCCACTAGAAGCTCTTCTGAGGGAGGTAATTAACAAACAGTGAATGGAA
AAACAGTGCTGTAGTCATCCTGTAATATGCTCCTGTCAACAATGTATACATTCTGCTAGG
TGCCATATTGCTTTAAGCTCAAGTCGCATCTTACTAGTGAAGTATTCTGCCAATGAAG
AAAACAAGTATGATTATCTTCCAACACTGTGAATGTGTGCTCAGAACTGGTGAAGCTAGTT
TTCTGTGTGCTTGTGTCAATCTGTGTTATAAAGAAAGATCATCAAAGTAGAAATTGAAATA
TGCTTCCTGGAAGGAATTCTCTGATTTATGAAGTGGTCCATTCTGCGCTTCTTTATTTCC
TGGATAACTTGATTGTCTTCTATGTCCTGTCTTCTTCAACCAGCCATGGCTGTTATCTTC
TCAAATTTTAGCATTATAACAACAGCTCTTCTATTTCAGGATAGTGTGAAGAGGCGTCTAAA
CTGGATCCAGTGGGCTTCCCTCTGACTTTATTTTGTCTATTGTGGCCTTACTGCCGGGA
CTAAACTTTA

FIGURE 11

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGCGCTTGCGTAGCGCGCGGCGGCC
 GTGGCTAAGGCTGCTACGAAGCGAGCTTGGGAGGAGCAGCGGCCCTGCGGGGCAGAGGAGCAT
 CCCGCTACCAAGTCCCAAGCGGCGTGGCCCCGCGGTCATGGCCAAAGGAGAAGGCCCGGAG
 AGCGGCTCCGCGGCGGGGCTGCTACCCACCAGCATCCTCCAAAGCACTGAACGCCCGGCCCA
 GGTGAAGAAAGAACCGAAAAAGAAGAAACAACAGTTGCTGTTTGCAACAAGCTTTGCTATG
 CACTTGGGGGAGCCCCCTACCAGGTGACGGGCTGTGCCCTGGGTTCTTCTCTCAGATCTAC
 CTATTGGATGTGGCTCAGGTGGGCCCTTTCTCTGCCCTCCATCATCCTGTTTGTGGGCGGAGC
 CTGGGATGCCATCAGACCCCCCTGGTGGGCGCTGTCATCAGCAAATCCCCCTGGACCTGCC
 TGGGTCGCGCTTATGCCCTGGATCATCTTCTCCACGCCCTGGCGCTCATGTGCCTACTTCTCT
 ATCTGGTTCGTGCGCGACTTCCACACGGCCAGACCTATTGGTACCTGCTTTTCTATTGCTCT
 CTTTGAACAATGGTCAGGTGTTTCCATGTTCCCTACTCGGCTCTCACCATGTTTCATCAGCA
 ACCGAGCAGACTGAGCGGGATTCTGCCACCGCCTATCGGATGACTGTGGAAGTGTGGGCAC
 AGTGCTGGGCACGGCGATCCAGGGACAAATCGTGGGCCAAGCAGACACGCTTGTTCACAG
 ACTTCAATAGCTCTACAGTAGCTTCACAAAGTGCCAACCATACACATGGCACCACTTCACAC
 AGGGAAACGCAAAAGGCATACCTGCTGGCAGCGGGGTCATTGTCTGTATCTATATAATCTG
 TGCTGTCATCTGATCCTGGGCGTGCAGGAGCAGAGAGAACCCTATGAAGCCAGCAGTCTG
 AGCCAATCGCCTACTTCCGGGGCTACGGCTGGTTCATGAGCCACGGCCCATACATCAAAT
 ATTACTGGCTTCTCTTACCTCCTTGGCTTTTATGCTGGTGGAGGGAACTTTGTCTGTT
 TTGCACCTACACCTTGGGCTTCCGCAATGAATCCAGAATCTACTCCTGGCCATCATGCTCT
 CGGCCACTTTAAACCATCCCATCTGCGAGTGGTTCTTGACCCGCTTGGCAAGAAGACAGCT
 GTATATGTTGGGATCTCATCAGCAGTGCCATTTCTCATCTTGGTGGCCCTCATGGAGAGTAA
 CCTCATATTACATATGCGGTAGCTGTGGCAGCTGGCATCAGTGTGGCAGCTGCCTTCTTAC
 TACCCTGGTCCATGCTGCCTGATGTGATTGACGACTTCCATCTGAAGCAGCCCCACTTCCAT
 GGAACGAGCCCATCTTCTTCTCTTCTATGTCTTCTTCACCAAGTTTGCTCTGGAGTGTG
 ACTGGGCATTTCTACCCTCAGTCTGGACTTGCAGGGTACCAGACCCGTGGCTGCTCGCAGC
 CGGAACGTGTCAAGTTTACTACTGAACATGCTCGTGACCATGGCTCCCATAGTTCTCATCCTG
 CTGGGCTGCTGCTCTTCAAAATGTACCCATTGATGAGGAGAGGCGGCGGCAAGATAAGAA
 GGCCCTGCAGGCACTGAGGGACGAGGCCAGCAGCTCTGGCTGCTCAGAAACAGACTCCACAG
 AGCTGGCTAGCATCCTCTAGGGCCCCGACGTTGCCCGAAGCCACCATCAGAGAAGGCCACAG
 AAGGGATCAGGACCTGTCTGCCGGCTTGCTGAGCAGCTGGACTGAGGTGCTAGGAAGGGA
 CTGAAGACTCAAGGAGGTGGCCCCAGGACACTTGCTGTGCTCACTGTGGGCGCGCTGCTCTG
 TGGCTCTGCTCTCCCTCTGCCTGCTGTGGGCGCAAGCCCTGGGGCTGCCACTGTGAATA
 TGCCAAGCACTGATCGGGCTAGCCGGAACACTAATGTAGAAACCTTTTTTTTACAGAGCC
 TAATTAATAACTTAATGACTGTGTACATAGCAATGTGTGTATGTATATGTCTGTGAGCTA
 TTAATGTTATTAATTTTCATAAAAGCTGGAAAGC

FIGURE 13

GGGAAACGCAAAGGCATACCTGCTGGCAGCGGGGGTCATTGTCTGTATCTATATAATCTGT
GCTGTGCATCCTGATCCTGGGCGTGCGGGAGCAGAGAGAACCCTATGAAGCCCAGCAGTCTGA
GCCAATCGCCTACTTCCGGGGCCTACGGCTGGTCATGAGCCACGGGCCATACATCAAACCTTA
TTACTGGCTTCCTCTTACCTCCTTGGCTTTCATGCTGGTGGAGGGGAACCTTGTCTTGTTT
TGCACCTACACCTTGGGCTTCCGCAATGAATTCCAGAATCTACTCCTGGCCATCATGCTCTC
GGCCACTTTAACCATTCCCATCTGGCAGTGGTTCTTGACCCGGTTTGGCAAGAAGACAGCTG
TATATGTTGGGATCTCATCAGCAGTGCCATTTCTCATCTTGGTGGCCCTCATGGAGAGTAAC
CTCATCATTACATATGCGGTAGCTGTGGCAGCTGGCATCAGTGTGGCAGCTGCCTTCTTACT
ACCCTGGTCCATGCTGCCTGATGTATTGACGACTTCCATCTGAAGCAGCCCCACTTCCATG
GAACCGAGCCCAT

FIGURE 14

GGGGCTTCGGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGGATTACAAAAGGTGCAGGT
 ATGAGCAGGTCTGAAGACTAACATTTTGTGAAGTTGTAAACAGAAAACCTGTTAGAAATGT
 GGTGGTTTCAGCAAGGCTCAGTTTCCTTCCTTCAGCCCTTGTAATTTGGACATCTGCTGCT
 TTCATATTTTCATACATTACTGCAGTAACACTCCACCATATAGACCCGGCTTTACCTTATAT
 CAGTGACACTGGTACAGTAGCTCCAGAAAAATGCTTATTTGGGGCAATGCTAAATATTGCGG
 CAGTTTTATGCATTGCTACCATTATGTTTCGTTATAAGCAAGTTCATGCTCTGAGTCCTGAA
 GAGAACGTTATCATCAAATTAACAAGGCTGGCCTTGTAAGTGAATACTGAGTTGTTTAGG
 ACTTTCTATTGTGGCAAACCTCCAGAAAACAACCCCTTTTGCTGCACATGTAAGTGGAGCTG
 TGCTTACCTTTGGTATGGGCTCATTATATATGTTTGTTTCAGACCATCCTTTCCTACCAAATG
 CAGCCCAAAATCCATGGCAAACAAGTCTTCTGGATCAGACTGTTGTTGGTTATCTGGTGTGG
 AGTAAGTGCAGTTAGCATGCTGACTTGCTCATCAGTTTTCACAGTGGCAATTTTGGGACTG
 ATTTAGAACAGAACTCCATTGGAACCCCGAGGACAAAGGTTATGTGCTTCACATGATCACT
 ACTGCAGCAGAATGGTCTATGTCATTTTCCTTCTTTGGTTTTTTCCTGACTTACATTTCGTGA
 TTTTCAGAAAATTTCTTTACGGGTGGAAGCCAATTTACATGGATTAACCTCTATGACACTG
 CACCTTGCCCTATTAACAATGAACGAACACGGCTACTTTCAGAGATATTTGATGAAAGGAT
 AAAATATTTCTGTAATGATTATGATTCTCAGGGATTGGGGAAAGGTTACAGAAGTTGCTTA
 TTCTTCTCTGAAATTTCAACCACTTAATCAAGGCTGACAGTAACACTGATGAATGCTGATA
 ATCAGGAAACATGAAAGAAGCCATTTGATAGATTATTTCTAAAGGATATCATCAAGAAGACTA
 TTAAAAACCTATGCCTATACTTTTTATCTCAGAAAATAAAGTCAAAAGACTATG

FIGURE 15

MWWFQQGLSFLPSALVIWTSAAFIFSYYITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNI
AAVLCIATYYVRYKQVHALSPEENVIIKLNKAGLVLGILSCLGLSIVANFQKTTLFAAHVSG
AVLTTFMGSLYMFVQTILSYQMOPKIHGKQVFWIRLLLVWCGVSALSMLTCSSVLHSGNFG
TDLEQKLHWNPEDKGYVLHMITTAAEWSMSFSFFGFFLTYYIRDFQKISLRVEANLHGLTLYD
TAPCPINNERTRLRSRDI

0991181.11501

FIGURE 16

CGGACGCTTGGGCNGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGTGCCTGATGCCGAGT
TCCGTCTCTCGGGTCTTTTCTGGTCCCAGGCCAAAGCGGAGCGGAGATCCTCAAACGGCCTA
GTGCTTCGCGCTTCCGGAGAAAATCAGCGGTCTAATTAATTCCTCTGGTTGTTGAAGCAGT
TACCAAGAATCTTCAACCCTTTCCCACAAAAGCTAATTGAGTACACGTTCTGTTGAGTACA
CGTTCCTGTTGATTTACAAAAGGTGCAGGTATGAGCAGGTCTGAAGACTAACATTTTGTGAA
GTTGTAAACAGAAAACCTGTTAGAAATGTGGTGGTTTCAGCAAGGCCTCAGTTTCCTTCCT
TCAGCCCTTGTAATTTGGACATCTGCTGCTTTCATATTTTCATACATTACTGCAGTAACACT
CCACCATATAGACCCGGCTTTACCTTATATCAGTGACACTGGTACAGTANC

FIGURE 17

CCCACGCGTCCGCCCGCCGCTGCGTCCCGAGTGCAAGTGAGCTTCTCGGCTGCCCGCGGG
 CCGGGGTGCGGAGCCGACATGCGCCCGCTTCTCGGCTCCTTCTGGTCTTGC CGCGGTGCAC
 CTTGCGCTTGTA CTTGCTGTGACGCGACTGCCCGCGGGCGGAGACTGGGCTCCACCGAGG
 AGGCTGGAGGCAGGTGCTGTGGTCCCCCTCCGACCTGGCAGAGCTGCGGGAGCTCTCTGAG
 GTCCTTCGAGAGTACCGGAAGGAGCACCAGGCCACGTGTTCTGCTCTTCTGCGGCGCCTA
 CCTCTACAAACAGGGCTTTGCCATCCCCGGCTCCAGCTTCTGAATGTTTTAGCTGGTGCCT
 TGTTTGGGCCATGGCTGGGGCTTCTGCTGTGCTGTGTGTTGACCTCGGTGGGTGCCACATGC
 TGCTACCTGCTCTCCAGTATTTTTGGCAAACAGTTGGTGGTGTCTACTTTCCTGATAAAGT
 GGCCCTGCTGCAGAGAAAGGTGGAGGAGAACAGAAACAGCTTGTTTTTTTCTTATTGTTTT
 TGAGACTTTTCCCATGACACCAAACCTGGTCTTGAACCTCTCGGCCCAATTCTGAACATT
 CCCATCGTGAGTTCTTCTTCTCAGTTCTTATCGGTTTGATCCCATATAATTTTCATCTGTGT
 GCAGACAGGGTCCATCCTGTCAACCCTAACCTCTCTGGATGCTCTTTTCTCCTGGGACACTG
 TCTTTAAGCTGTTGGCCATTGCCATGGTGGCATTAAATTCCTGGAACCCCTCATTA AAAAATT
 AGTCAGAAACATCTGCAATTGAATGAAACAAGTACTGCTAATCATATACAGTAGAAAAGA
 CACATGATCTGGATTTTCTGTTTGCCACATCCCTGGACTCAGTTGCTTATTTGTGTAATGGA
 TGTGGTCTCTAAAGCCCTCATTTGTTTTGATTGCCCTTCTATAGGTGATGTGGACACTGTG
 CATCAATGTGCAGTGTCTTTTCAGAAAGGACACTCTGCTCTTGAAGGTGATTACATCAGGT
 TTTCAAACAGCCCTGGTGTAGCAGACACTGCAACAGATGCCTCCTAGAAAAATGCTGTTTGT
 GGCCGGGCGCGGTGGCTCACGCCGTGAATCCAGCACTTTGGGAGGCCGAGGCCGGTGATT
 ACAAGGTCAGGAGTTCAAGACCAGCCTGGCCAAGATGGTGAAATCCTGTCTCTAATAAAAAAT
 ACAAAAAATTAGCCAGGCGTGGTGGCAGGCACCTGTAATCCAGCTACTCGGGAGGCTGAGGC
 AGGAGAATTGCTTGAACCAAGGTGGCAGAGGTTGCAGTAAGCCAAGATCACACCACTGCACT
 CCAGCCTGGGTGATAGAGTGAGACACTGTCTTGAC

FIGURE 18

MRPLLGLLLVFAGCTFALYLLSTRLPGRRLGSTEEAGGRSLWFPSDLAELRESEVLREYR
 KEHQAYVFLLFCGAYLYKQGFAIPGSSFLNVLAGALFGPWGLLLCCVLTSGATCCYLLSS
 IFGKQLVVSYPDPKVALLRKVEENRNSLFFLLFLRLFPMTPNWFLNLSAPILNIPIVQFF
 FSVLIGLIPYNFICVQTGSILSTLTSLDALFSWDTVFKLLAIAMVALIPGTLIKKFSQKHLQ
 LNETSTANHIHSRKDT

Important features:**Signal peptide:**

amino acids 1-17

Transmembrane domains:

amino acids 101-123, 189-211

N-glycosylation sites.

amino acids 172-176, 250-254

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 240-244, 261-265

N-myristoylation site.

amino acids 13-19, 104-110, 115-121, 204-210

Amidation site.

amino acids 27-31

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 4-15

Protein splicing proteins.

amino acids 25-31

Sugar transport proteins.

amino acids 162-172

FIGURE 19

CCGAGGCGGGAGGAGCCCCGAGGGGCGCGAGCCCCGATGAATCATTGTAGTCAATCATTTT
 CCAGTTCCTCAGCCGCTCAGTTGTGATCAAGGGACACGTGGTTTCCGAAGTCCAGCTCAGAA
 TAGGAAAATAACTTGGGATTTTATATTGGAAGAC**ATGG**GATCTTGCTGCCAACGAGATCAGCA
 TTTATGACAACTTTCAGAGACTGTTGATTTGGTGAGACAGACCGGCCATCAGTGTGGCATG
 TCAGAGAAGGCAATTGAAAAATTTATCAGACAGCTGCTGGAAAAGAAATGAACCTCAGAGACC
 CCCCCGCAGTATCCTCTCCTTATAGTTGTGTATAAGGTTCTCGCAACCTTGGGATTAATCT
 TGCTCACTGCCTACTTTGTGATTCAACCTTTCAGCCCATTAGCACCTGAGCCAGTGCTTTCT
 GGAGCTCACACCTGGCGCTCACTCATCCATCACATTAGGCTGATGTCCTTGCCCATTGCCAA
 GAAGTACATGTCAGAAAATAAGGGAGTTCCTCTGCATGGGGGTGATGAAGACAGACCTTTC
 CAGACTTGGACCCCTGGTGGACAAACGACTGTGAGCAGAATGAGTCAGAGCCCATTCTGCC
 AACTGCACTGGCTGTGCCCAGAAACACCTGAAGGTGATGCTCCTGGAAGACGCCCCAAGGAA
 ATTTGAGAGGCTCCATCCACTGGTGATCAAGACGGGAAAGCCCCCTGTTGGAGGAAGAGATTC
 AGCATTTTTTGTGCCAGTACCCTGAGGCGACAGAAGGCTTCTCTGAAGGGTTTTTCGCCAAG
 TGGTGGCGCTGCTTCTCTGAGCGGTGGTCCCATTTCCTTATCCATGGAGGAGACCTCTGAA
 CAGATCACAAATGTTACGTGAGCTTTTCTCTGTTTTCCTCACCTGCCATTTCCAAAAGATG
 CCTCTTTAAACAAGTGCTCCTTCTTCACCCAGAACCTGTTGTGGGGAGTAAGATGCATAAG
 ATGCCCTGACCTATTTATCATTGGCAGCGGTGAGGCCATGTTGCAGCTCATCCCTCCCTTCCA
 GTGCCGAAGACATTGTCAGTCTGTGGCCATGCCAATAGAGCCAGGGGATATCGGCTATGTGG
 ACACCCCACTGGAAGGTCTACGTTATAGCCAGAGGGGTCCAGCCTTTGGTCATCTGCGAT
 GGAACCGCTTTCTCAGAAGCT**GTAG**GAAATAGAACTGTGCACAGGAACAGCTTCAGAGCCGA
 AAACCAGGTTGAAAGGGGAAAAATAAAAAACAAAACGATGAAACTGCAAAAA

FIGURE 20

MDLAANEISYDKLSETVDLVRQTGHQCGMSEKAIEKFIRQLLEKNEPQRPPQYPLLIVVY
KVLATLGLILLTAYFVIQPFSPPLAEPVLSGAHTWRSLIHHIRLMSLPIAKKYMSENKGVPL
HGGDEDRPFPDFDPWWTNDCEQNESEPIPANCTGCAQKHLKVMLLEDAPRKFERLHPLVIKT
GKPLLEEEIQHFLCQYPEATEGFSEGGFFAKWWRCFPERWFFPYPWRRLNRSQMLRELFPV
FTHLPFPKDASLNKCSFLHPEPVVGSKMHKMPDLFIIGSGEAMLQLIPPFQCRRHCSVAMP
IEPGDIGYVDTHWKVYVIARGVQPLVICDTAFSEL

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FIGURE 21

CCACGGTGTCGGTTCTTCGCCCCGGCGGCAGCTGTCCCCGAGGCGGGAGGAGCCCCGAGGGGCG
CGAGCCCCGCATGAATCATTGTAGTCAATCATTTTCAGTTCTCAGCCGTTTCAGTTGTGATC
AAGGGACACGTGGTTTCCGAACTGCCAGCTCAGAATAGGAAAATAACTTGGGATTTTATATT
GGAAGACATGGATCTTGCTGCCAACGAGATCAGCATTTATGACAACTTTCAGAGACTGTTG
ATTTGGTGAGACAGACCGGCCATCAGTGTGGCATGTCAGAGAAGGCAATTGAAAAATTTATC
AGACAGCTGCTGAAAAAGAATGAACCTCAGAGACCCCCCGCAGTATCCTCTCCTTATAGT
TGTGTATAAGGTTCTCGCAACCTTGGGATTAATCTTGCTCACTGCCTACTTTGTGATTC AAC
CTTTCAGCCATTAGCACCTGAGCCAGTGCTTTGTGGAGCTCAC

090134 71601

FIGURE 22

CCCACGCGTCCGCCACGCGTCCGGCTGAACACCTCTTCTTTGGAGTCAGCCACTGATGAGG
 CAGGGTCCCCACTTGCAGCTGCAGCAGCTGCAGCAGCTGCAGAGCGCTGCTCCTGGCTGGTG
 CCACTGGTGCACCGCTGCTAGACCGTGCTATGAGCCGCTGGGGCTGCAGTGGGACTGCC
 CTCCTGCCACCCACCAATGGCAGCCCCACCTTCTTTGAAGACTTCCAGGCTTTTTGTGCCA
 CACCCGAATGGCGCCACTTTCATCGACAAACAGGTACAGCCAAC**ATG**TCCAGGTTTCGAAATG
 GACACGATGCTAAGAGCCAGCAGCTTATGTCAAGTTTCTGGAATGCCCTGCTATGCATGCT
 TATGACATGGGCGCAGCGGCCAGTGGGAGCGCGCCAGAGCTCGTCGGGCCCTTCCAGGAGC
 TGGTGCTGGAACCTGCGCAGAGGCGGGCGCGCTGGAGGGGCTACGCTACACGGCAGTGCTG
 AAGCAGCAGGCAACGCAGCACTCCATGGCCCTGCTGCACTGGGGGGCGCTGTGGCGCCAGCT
 CGCCAGCCCATGTGGGGCCTGGCGCTGAGGGACACTCCCATCCCCCGCTGGAAACTGTCCA
 GCGCCGAGACATATTACGCATGCGTCTGAAGCTGGTGCCCAACCATCACTTCGACCCTCAC
 CTGGAAGCCAGCGCTCTCCGAGACAATCTGGGTGAGGTTCCCTGACACCCACCAGGAGGCG
 CTCACCTGCTTGGCCATGACCAAGAGGCGAAAGTGAACCCCCAGGAGTTGCTGCAAGG
 AGGACCACTCGGGCAGGACGAGCTGGCTGAGCTGGAGACCCCGATGGAGGCGAGCAAACTG
 GATGAGCAGCGTGAGAAGCTGGTGCTGTCGGCCGAGTGCCAGCTGGTGACGGTAGTGGCCGT
 GGTCCAGGGCTGCTGGAGGTCAACACAGAAATGTATACTTCTACGATGGCAGCACTGAGC
 GCGTGGAACCCGAGGAGGCGCATCGGCTATGATTTCCGGCGCCCATGGCCAGCTGCGTGAG
 GTCCCACTGCGGCTTTCAACCTGCGCGCTTCAGCACTTGAGCTCTTCTTTATCGATCGAGG
 CAACTACTTCTCAACTTCCCATGCAAGGTGGGCGAGCCAGTCTCATCTCTTAGCCAGA
 CTCGAGACACCCAGCCTGGCCCCATCCCACCCCATACCCAGGTACGGAACCAAGGTGTAATCG
 TGCGCTCTGCGCTTACGCCCCCTCTCAAGGCTACCTAAGCAGCCGCTCCCCCAGGAGAT
 GCTGCGTGCTCAGGCCTTTACCAGAAATGGGTACAGCGTGAGATATCCAACCTTCAGTACT
 TGATGCACTCAACACCACTTGGGGGCGGACCTACAATGACCTGTCTCAGTACCTGTGTTCT
 CTTGGGTCTCTCAGGACTACGTGTCCCCAACCTTGACCTCAGCAACCCAGCCGCTTCTCCG
 GGACCTGTCTTAAGCCCTCTGGTGTGGTGAACCCCAAGCATGCCAGCTCGTGAGGGAGAAGT
 ATGAAAGCTTTGAGAGCCAGCAGGGACCAATGACAAGTTCACCTATGGCACCCTACTCTCC
 AATGACCGCTGATGCACACTACTCATCCGCTGGAGCCCTTACCTCCCTGGCTGCCA
 GCTGCAAGTGGCCGCTTTGACTGCTCCGACCGCAGTTCCACTCGGTGGCGGCGAGCTGGC
 AGGCACGCTGGAGAGCCTGCCGATGTGAAGGAGCTCATCCCGAAATTCCTTACTTTCTCT
 GACTTCTTGAGAAACAGAACCGTTTTGACTGGGCTGTCTCCAGCTGACCAACGAGAAGGT
 AGGCGATGTGGTGCTACCCCGTGGGCCAGCTCTCCTGAGGACTTCATCCAGCAGCACCGCC
 AGGCTCTGGAGTCGGAGTATGTGCTGCACACCTACACGAGTGGATCGACCTCATCTTTGGC
 TACAAGCAGCGGGGGCCAGCCGCCGAGGAGGCCCTCAATGTCTTCTATTACTGCACCTATGA
 GGGGGCTGTAGACTGGACCATGTGACAGATGAGCGGGAACGGAAGGCTCTGGAGGGCATTA
 TCAGCAACTTTTGGGAGACTCCCTGTCACTGTGTAAGGAGCCACATCCAACCTCGGCTTCA
 CTTGGAGGAGCAGCCCATCGCCTTGACGCTGGACACTAATCACTCAGCTAGCATCTTCCAGCA
 CTTGGAAGCACTCAAGGCATTTCTCGCAGAGGTGACTGTGAGTGCCAGTGGGCTGCTGGGGA
 CCCACAGCTGGTTGCCCTATGACCGCAACATAAGCAACTACTTCACTTCAGCAAAAGACCCC
 ACCATGGGCAAGCCAAAGACGACGCACTGCTGAGTGGCCCTGGGTGCCAGGCTGGTGT
 GAGTGGACAAGCACTGGCAGTGGCCCCGATGGAAGCTGCTATTCAAGCGGTGGCCACTGGG
 ATGGAGCCTGCGGGTGACTGCACACTACCCCGTGGCAAGCTGTTGAGCCAGCTCAGCTGCCAC
 CTTGATGTAGTAACCTGCCTTGCACTGGACACTGTGGCATCTACCTCATCTCAGGCTCCCG
 GGACACCAAGCTGCATGGTGTGGCGGCTCCTGCATCGGTGGTCTGTGTAGTGGCTGGCAC
 CAAAGCCTGTGCAGGTCTGCTATGGGCATGGGGCTGCAGTGAAGCTGTGTGGCCATCAGCAT
 GAACCTGACATGCTGTGCTCTGGATCTGAGGATGGAAGTGTGATCATACACACTGTACGCCG
 CGGACAGTTTGTAGCGGCACACTCGGCCCTCTGGGTGCCACATTCCTTGGAACCTATTTGCCAC
 TGGCATTTGGGCTCCGAAGGCCAGATTGTGGTACAGAGCTCAGCGTGGGAAGCTCTTGGGGCC
 CAGGTCACTACTCTTGCACCTGTATTGATCAATGGGAAGTTGGCGGCTTCACTGGCCCCCT
 GGCAGAGCAGCTCAGCGCTGACGGTGACAGAGGAGCTTGTGTTGCTGGGCGAGCCGCCAGT
 GCGCCCTGCACTCTCCAATAAACACACTGCTCCCGGCCGCGCTCCCTTGCCCATGAAG
 GTGGCCATCCGAGCTGCGCGTGACCAAGGAGCGCAGCCAGTGTGTTGGGCTGGAGG
 TGGAAGCTCATCTGCTGGTGGTGGCGGGGAGCCCTCTGAGGTGGCAGAGCCAGCTGCGCG
 GGAAGTGTGGCGGTGTGTCGCGGCGCATCTCCAGGTGTCTCGGAGAGCAGGAATACAAC
 CCTACTGAGCGCGCT**GA**CACTGGCCAGTCCGCGCTGCTCGGGCCCGCCCCCGCAGGCGCTG
 GCGCGGAGGCCCCCGAGAAAGTCGGCGGGAACACCCCGGGCGAGCCAGCCAGGGGGTGA
 GCGGGGCCACCTGCGCAGCTCAGGATTGGCGGGCGATGTTACCCCTCTCAGGATTTGGG
 GCGGGAAGTCCCGCCCTCGCGGCTGAGGGGCGCCCTGAGGGCGAGCTGGCGCT

FIGURE 23

MSQFEMDTYAKSHDLMMSGFWNACYDMLMSSGQRRQWERAQSRRAFQELVLEPAQRRARLEGL
 RYTAVLKQQATQHSMALLHWGALWRQLASPCGAWALRDTPIPRWKLSAETYSRMRLKLVPN
 HHFDPHLEASALRDNLGEVPLTPTEEASLPLAVTKEAKVSTPPELLQEDQLGEDELALETF
 MEAAELDEQREKLVLSAECQLVTVVAVVPGLLVTTQNVYFYDGSTERVETEEGIGYDFRRP
 LAQLREVHLRRFNLRSALELFFIDQANYFLNFFCKVGTTPVSSSQTPRPQPGPIPPHTQV
 RNQVYSWLLRLRPSSQGYLSSRSPOEMLRASGLTQKVVQREISNFEYLMQLNTIAGRTYNDL
 SQYPVFPWVLQDYVSPTLDLSNPAVFRDLSKPIGVVNPKHAQLVREKYESFEDPAGTIDKFH
 YGTHYSNAAGVMHYLIRVEPFTSLHVQLQSGRFDSCDRQFHSVAAAWQARLESPADVKEILP
 EFFFYFPDFLENQNGFDLGCGLTNEKVGDVVLPWASSPEDFIQHRQALESEYVSAHLHEW
 IDLIFGYKQRGPAEEALNVFYCYEGAVDLHDVTDERERKALEGIIISNFGQTPCQLLKEP
 HPTRLSAEEAAHRLARLDTNPSPIFQHLDELKAFFAEVTVSASGLLGTHSWLPYDRNISNYF
 SFSKDPMTGSHKTRQLLSGPPVPGSGVSGQALAVAPDGKLLFSGGHWGDSLRVTALPRGKLL
 SQLSCHLDVVTCLALDTCGIYILISGRDTCMVWRLHQQGLSVGLAPKVPQVLYGHGAAYS
 CVAISTELDMAVSGSEDTGVIHTVRRGQFVAALRPLGATFPGPIFHLALGSEGQIVVQSSA
 WERPQAQVTYSLHLYSVNGKLRASLPLAEQPTALTVTEDFVLLGTAQCALHILQLNTLLPAA
 PPLPMKVAIRSAVTKERSHVLVGLEDKLIVVAGQPSEVRSSQFARKLWRSSRRISQVSS
 GETEYNPTAR

N-glycosylation site.

amino acids 677-681

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 985-989

Tyrosine kinase phosphorylation site.

amino acids 56-65, 367-376, 543-551

N-myristoylation site.

amino acids 61-67, 436-442, 604-610, 610-616, 664-670, 691-697,
 706-712, 711-717, 769-775, 785-791, 802-808, 820-826, 834-840,
 873-879, 912-918, 954-960

FIGURE 24

CGGACGCGTGGGCGGACGCGTGGGGGCTGTGAGAAAGTGCCAATAAATACATCATGCAACCC
 CACGGCCACCTTGTGAACCTCTCGTGCCAGGGCTGATGTGCGTCTTCCAGGGCTACTCAT
 CCAAAGGCTAATCCAACGTTCTGTCTTCAATCTGCAAAATCTATGGGGTCTGGGGCTCTTC
 TGGACCCCTTAAC TGGGTACTGGCCCTGGGCCAATGCGTCTCTCGTGGAGCCTTTGCCTCCTT
 CTACTGGGCCTTCCACAAGCCCCAGGACATCCCTACCTTCCCCCTTAATCTCTGCCTTCATCC
 GCACACTCCGTTACCACACTGGGTCATTGGCATTGGAGCCCTCATCTGACCCTTGTGCAG
 ATAGCCCCGGTTCATCTTGGAGTATATTGACCACAAGCTCAGAGGAGTGCAGAACCCTGTAGC
 CCGCTGCATCATGTGCTGTTTCAAGTGCTGCCCTCTGGTGTCTGGAAAAATTTATCAAGTTCC
 TAAACCGCAATGCATACATCATGATCGCCATCTACGGGAAGAATTTCTGTGTCTCAGCCAAA
 AATGCGTTTACGTACTCATGCGAAACATTGTCAGGGTGGTCGTCTTGACAAAGTCACAGA
 CCTGTGCTGTTCTTTGGGAAGCTGCTGGTGGTCGGAGGCGTGGGGGTCTGTCTCTCTTTT
 TTTTCTCCGTCGCATCCCGGGCTGGGTAAAGACTTTAAGAGCCCCACCTCAACTATTAC
 TGGCTGCCCATCATGACCTCCATCCTGGGGGCTATGTATCGCCAGCGGCTTCTTCAGCGT
 TTTCCGCATGTGTGTGGACACGCTCTTCTCTGCTTCTGGAAGACCTGGAGCGGAACAACG
 GCTCCTTGGACCGGCCCTACTACATGTCCAAGAGCCTTCTAAAGATTCTGGGCAAGAAGAAC
 GAGGCGCCCCCGACAACAAGAAGAGGAAGAAGTGAAGCTCCGGCCCTGATCCAGGACTGC
 ACCCCACCCACCGTCCAGCCATCCAACCTCACTTCGCCTTACAGGTCTCCATTTTGTGGT
 AAAAAAAGGTTTTAGGCCAGGCGCGTGGCTCACGCCGTGTAATCCAACACTTTGAGAGGCTG
 AGGCGGGCGGATCACCTGAGTCAGGAGTTCGAGACCAGCCTGGCCAACATGGTGAACCTCC
 GTCTCTATTAAAAATACAAAATTAGCCGAGAGTGGTGGCATGCACCTGTCATCCCAGCTAC
 TCGGAGGCTGAGGCAGGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTGAGCCGAGA
 TCGCGCCACTGCACTCCAACCTGGGTGACAGACTCTGTCTCCAAAACAAAACAAACAA
 AAAGATTTTATTAAAGATATTTTGTTAACCTC

FIGURE 26

GAGTCTTGACCGCCGCCGGGCTCTTGGTACCTCAGCGCAGCGCCAGGCGTCCGGCCCGCGT
 GGCTATAGTTCGTGTCCGATTTCGCGAAAGAGTTCTACGAGGTGGTCCAGAGCCAGAGGGTCC
 TTCTCTTCGTGGCCTCGGACGTGGATGCTCTGTGTGCGTGCAAGATCCTTCAGGCCCTGTTC
 CAGTGTGACCACGTGCAATATACGCTGGTCCAGTTTCTGGGTGGCAAGAAGTGAAGTGC
 ATTTCTTGAGCATAAAGAAGAGTTTCATTATTTTATTCTCATAACTGTGGAGCTAATGTAG
 ACCTATTGGATATTCTTCAACCTGATGAAGACACTATATTCTTTGTGTGACTCCCATAGG
 CCAGTCAATGTGCTCAATGTATACAACGATACCCAGATCAAATTACTCATTAAACAAGATGA
 TGACCTTGAAGTTCCCGCCTATGAAGACATCTTCAGGGATGAAGAGGAGGATGAAGAGCATT
 CAGGAAATGACAGTGATGGGTGAGAGCCTTCTGAGAAGCGCACACGGTTAGAAGAGGAGATA
 GTGGAGCAAACCATGCGGAGGAGGCAGCGCGAGAGTGGGAGGCCCGGAGAAGAGACATCCT
 CTTTGACTACGAGCAGTATGAATATCATGGGACATCGTCAGCCATGGTGATGTTTGAGCTGG
 CTTGGATGCTGTCCAAGACCTGAATGACATGCTGTGGTGGGCCATCGTTGGACTAACAGAC
 CAGTGGGTGCAAGACAAGATCACTCAAATGAAATACGTGACTGATGTTGGTGTCTGTCAGCG
 CCACGTTTCCCGCCACAACACCGGAACGAGGATGAGGAGAACACACTCTCCGTGGACTGCA
 CACGGATCTCCTTTGAGTATGACCTCCGCCTGGTGCTCTACCAGCACTGGTCCCTCCATGAC
 AGCCTGTGCAACACCAGCTATACCGCAGCCAGGTTCAAGCTGTGGTCTGTGCAATGGACAGAA
 GCGGCTCCAGGAGTTCCTTGACAGACATGGGTCTTCCCTGAAGCAGGTGAAGCAGAAGTCC
 AGGCCATGGACATCTCCTTGAAGGAGAATTGCGGGGAAATGATTGAAGAGTCTGCAAAATAAA
 TTTGGGATGAAGGACATGCGCGTGCAGACTTTAGCATTCATTTTGGGTTCAAGCACAAGTT
 TCTGGCCAGCGACGTGGTCTTTGCCACCATGTCTTTGATGGAGAGCCCCGAGAAGGATGGCT
 CAGGGACAGATCACTTCATCCAGGCTCTGGACAGCCTCTCCAGGAGTAACCTGGACAAGCTG
 TACCATGGCCTGGAACCTGCCAAGAAGCAGCTGCGAGCCACCCAGCAGACCATTGCCAGCTGC
 CTTTGACCAACCTCGTCATCTCCAGGGCCTTTCTGTACTGCTCTCTCATGGAGGGCAC
 TCCAGATGTCATGCTGTCTCTAGGCCGGCATCCCTAAGCCTGCTCAGCAAACACCTGCTCA
 AGTCCCTTTGTGTGTTCGACAAAGAACCAGCGCTGCAAACTGCTGCCCTGGTGATGGCTGCC
 CCCCTGAGCATGGAGCATGGCACAGTGACCGTGGTGGGCATCCCCCAGAGACCGACAGCTC
 GGACAGGAAGAACTTTTTGGGAGGGCGTTTGAGAAGGCAGCGGAAAGCACCAGCTCCCGGA
 TGCTGCACAACCATTTTGACCTCTCAGTAATTGAGCTGAAAGCTGAGGATCGGAGCAAGTTT
 CTGGACGCATTATTTCCCTCCTGTCTCTAGGAATTTGATTCTTCAGAATGACCTTCTTATT
 TATGTAAGTGGCTTTCATTTAGATTGAAGTTATGGACATGATTTGAGATGTAGAAGCCATT
 TTTTATTAATAAATGCTTATTTTAGGAAA

FIGURE 27

MFVSDFRKEFYEVVQSQRVLLFVASDVDALCACKILQALFQCDHVQYTLVPVSGWQELETAF
LEHKEQFHYFILINCGANVDLLDILQPDEDTIFVCDSHRFVNVVNVYNDTQIKLLIKQDDD
LEVPAVEDIFRDEEEDEEHSGNDS DGSEPSEKRTL EEEIVEQTMRRRQRREWEARRRDILF
DYEQYEHGTSSAMVMFELAWMLSKDLNDMLWWAIVGLTDQWVQDKITQMKYVTDVGVLQRH
VSRHNRNEDEENTLSVDCTRISFEYDLRLVLVYQHWSLHDSL CNTSYTAARFKLWSVHGQKR
LQEFLADMGLPLKQVKQKFQAMDISLKENLREMIEESANKFGMKDMRVQTF SIHFGFKHKFL
ASDVVFATMSLMESPEKDGSGTDHFIQALDSLRSNLDKLYHGLELAKKQLRATQQTIASCL
CTNLVISQGFFLYCSLMEGTPDVMLFSRPASLSLLSKHLLKS FVCSTKNRRCKLLPLVMAAP
LSMEHGTVTVVGIPPETDSSDRKNFFGRAFEKAAESTSSRMLHNF DLSVIELKAEDRSKFL
DALISLLS

000101-1101

FIGURE 28

GTACCTCAGCGCAGCGCCAGGCGTCCGGCCGCCGTGGCTATGNTCGTGTCCGATTTCGCA
AAGAGTTCTACGAGGTGGTCCAGAGCCAGAGGGTCCTTCTCTTCGTGGCCTCGGANGTGGAT
GCTCTGTGTGCGTGCAAGATCCTTCAGGCCTTGTTCCAGTGTGACCANGTGCAATATANGCT
GGTTCAGTTTCTGGGTGGCAAGAACTTGAAACTGCATTTCTTGAGCATAAAGAACAGTTTC
ATTATTTTATTCTCATAAACTGTGGAGCTAATGTAGACCTATTGGATATTCTTCAACCTGAT
GAAGACACTATATTCTTTGTGTGTGACCCATAGGCCAGTCAATGTTGTCAATGTATACAA
CGATACCC

009101-1101

FIGURE 29

CAGGAACCCCTCTCTTTGGGTCTGGATTGGGACCCCTTTCAGTACCATTATTTTCTAGTGAAC
 CACGAAGGGACGATACAGAAAAACCCCTCAACCCCAAAGGAAATAGACTACAGGCCCAATTG
 GCTGACTTTGGCTATAGAAAAAGAAAGGAACGAAAAGAGACAGTTTATTTTGGAAAGCTAA
 GTCTTCCCTTTATCGAGTCAAGAAACCCCCCTTCTTGAGCTATTACAGCTTTTAAACAATT
 GAGTAAAGTACGTTCCGGTCACCATGGTGACAGCCGCCCTGGGTCCCGTCTGGGCAGCGCTC
 CTGCTCTTTCTCTGATGTGTGAGATCCGTATGGTGGAGCTCACCTTTGACAGAGCTGTGGC
 CAGCGCTGCCAACCGTGTCTGACTCTGAGGACCCCTGGATCTCTGCCATGTATCTCTCAG
 CCTCTTCTCCGGCCGCCCCACGCCCTGCCTGAGATCAGACCCCTACATTAATATACCATC
 CTGAAGGGTGACAAAGGGGACCCAGGCCCAATGGGCCTGCCAGGGTACATGGGCAGGGAGGG
 TCCCCAAGGGGAGCCTGGCCCTCAGGGCAGCAAGGGTGACAAAGGGGAGATGGGCAGCCCCG
 GCGCCCCGTGCCAGAAGCGCTTCTTCGCCTTCTCAGTGGGCCGCAAGACGGCCCTGCACAGC
 GCGGAGGACTTCCAGACGCTGCTCTTCGAAAGGGTCTTTGTGAACCTTGATGGGTGCTTTGA
 CATGGCCACCGCCAGTTTGTCTGCTCCCTGCGTGGCATCTACTTCTTCAGCCTCAATGTGC
 ACAGCTGGAATTACAAGGAGAGCTACGTGCACATTATGCATAACAGAAAGAGGCTGTCTC
 CTGTACGCCGACCCAGCGAGCGACATCATGCAGCCAGAGTGTGATGCTGGACCTGGC
 CTACGGGGACCGCGTCTGGGTGCGGCTCTTCAAGCGCCAGCGCGAGAAGCCCATCTACAGCA
 ACGACTTCGACACCTACATCACTTCAAGCGCCACCTCATCAAGGCCGAGGACGACATGAGGG
 CCTCTGGGCACCCCTCCCGGCTGGAGAGCTCAGGTGCTGGTCCCCGTCCCTGCAGGGCTCAG
 TTTGCACTCTGTGAAGCAGGAAGGCCAGGGAGGTCCCCGGGACTTGGCACTCTGGGGAGA
 CCTGCTCTTCTATCTTGGCTGCCATCATCCTCCAGGCTATTCTCTGCTCTCTCTCTCTCTCT
 TGGACCTATTTTAAAGACTTGTCAACCTAAATATTCTAGAACTTTCCAGCCTCGTAGGCC
 AGCATTCTCAAATCTGGAATGCATGCCAATCACCGGGGTTCGTGTTAAATGCAGATTCT
 GACTCAGCAGCTTCTGAGTGGGTCCAGGATTCTGTGTTTCTCATATGTTCTGGGTGATGCTG
 ATGGGGTCACTCTATGAACCACTGGAGCAACAGGTTCTAGGACTTTCTCAATATTCTAG
 TACTTTCTGAACATTTCTGGAATCTCTCCACATTCTAGAATTCTCCCAACATTTTTTTTCT
 TGAGACAGACTCTTGCTCTGTTGCCAGGCTAGAGTGCAGTGGTGCAATCTCAGTTCACTGC
 AACCTCTGCTCCCGGGTTCAAGCGATTCTTCTGCCTCAGCCTCCCTAGTGGCTGGGATTAC
 AGGCGCTCTGTACCATGCTGGCTAATTTTGTATTTTGTAGAGATGGGGTTTACCATA
 TTGGCCAGGCTGGTCTTGAACCTCTGACTTCAGGTGACCCACCCGCTCGGCCCTCAAAAT
 GCTGGGATTCAGAGTGTGAGCCACCGTGCCTGGCCAAATCCAACATTCTTAAATTTCTCTAT
 CCTCCAGGGCTCCCGTGCTATGTTCTTTTACCCCTTCCCTCTTCTCTTCTTCTTCTCAGGCC
 TGACCACTGACGCCACCGTTCAATTATTCAATTCATTAAACACTGAGCACTCACTCTGTGCT
 GGTCCCGGGAAGGTGAGGGGTGAGACACAGGCCCTGCCCTGCCCTCAGTGAAGGCCCA
 GCTCAGGCCAGGCCGGGAGAGATGTGTACATAGGTTTTAAAGCAGACCCAGAGCTCTGGGG
 GCTGTGTTCTGGGTGTTCTCAGGTGCTGCTGGTCTCCATTACCCACTGCTCCCCAAGGCTGG
 TGGGACGGGTCCCGGTGGCAGGGGCGAGTATCTCCTTCCGCTTCTCATCCACTGCCCAAG
 TGCTCATCTGTTACAGCAAAACCCAGGGGCTTGGCCAGGTCAAGGGTTCTGTGAGGAGAGG
 ACCCAGGAGTGTGGGGCATTTGGGGGGTGAAGTGGCCCCGCAAGAATGGAACCCACACCA
 TAGCTCTCCCCACAGCTGATACGGCATCTCGCAGAAAGACCTGCCCTCACTCTGGGATCCC
 CTCTCTGCTCTCTCCAGGGCTCTGCCAGGGCCTTGGTCTCAGTCCCTTCCACCAAAGTCACT
 GAATCTCCGTTTCCCAAGGCCCTCCAGTGCCTCAGACACTGATGTCTGTCCCCAGGTGCT
 CTCTGCCCCCTCATGCCCCCTCAACGGCCAGTCCCCGACTCTCCAGGCTTTTACAGGTG
 CTAAGGCCCGGTGGGCGACCTCTCGTCTCAGAGCCCTTCCCGGCTGGTGTGCTGCTTTAC
 AAACACTGCAAGGAGAAGGGCCACGGAAGCCCCAGGCTTTAGAGCCCTCAGCAGGTCTGGGG
 AGCTAGAGCAAAAGGAGGACCTCAGGCCTTCCGTTTCTTCCAGGGTGGGGTGGCTTGT
 GTTCCCTAGCTCTCAAAACCCAGGTGGCTGCCCTTCTCCCCAGAGGAGGGCCCTCCCG
 CCATTGGTGCTCATGACAGCTTGGGCTGAGGTGCCCGGGGGTGTATCTCTGGTGTCTAC
 AGCCGAGGGAGCCGTGGCTCCATGGCCAGATGACGGAACAGGGTCTGACCAAGTGGCAGGA
 AGACTGTGCTATAAACACCCCTGCCTGATCTGCCCTGCTGACCCGCCAGCCCTGCC
 GTCCAGCATGATTAAAGATGCTGTCTCTCTTGGAAAAAAGAAAAA

099131.11601

FIGURE 30

MVTAALGPVWAALLLFLLMCEIRMVELTFDRAVASGCQRCCDSEDPLDPAHVSSASSSSGRPH
ALPEIRPYINITILKGDKGDPGPMGLPGYMGREGPGQGEPGFPQGSKDGKMGEMSGAPCQKRF
FAFSVGRKTALHSGEDFQTLLFERVFNLDGCFDMATGQFAAPLRGIYFFSLNVHSWNYKET
YVHIMHNQKEAVILYAQPSPERSIMQSQSVMLDLAYGDRVVRLFKRQRENAIYSNDFDTYIT
FSGHLIKAEDD

Important features:**Signal peptide:**

amino acids 1-20

N-glycosylation site.

amino acids 72-75

Clq domain proteins.

amino acids 144-178, 78-111 and 84-117

FIGURE 33

GAATCATCCACGCACCTGCAGCTCTGCTGAGAGAGTGCAAGCCGTGGGGGTTTTGAGCTCAT
 CTTCATCATTCATATGAGGAATAAGTGGTAAAAATCCTTGGAAAAATGCAATGAGACTCATCAG
 AAACATTTTACATATTTTGTAGTATTGTTATGACAGCAGAGGTTGATGCTCCAGAGCTGCCAG
 AAGAAAGGGAATCATGATGACCAACTGCTCCAACATGCTCTAAGAAAGGTTCCCGCAGACTTG
 ACCCGGCCACAACGACACTGGATTATCTATAACCTCCTTTTCAACTCCAGAGTTTCAGA
 TTTTCATTCTGTCTCCAAACTGAGAGTTTTGATTCTATGCCATAACAGAAATCAACAGCTGG
 ATCTCAAACCTTTGAATTTCAACAAGGAGTTAGATATTAGATTGTCTAATAACAGACTG
 AAGAGTGTAACTTGGTATTTACTGGCAGGTCTCAGGTATTAGATCTTTCTTTTAAATGACTT
 TGACAGCCAAAAATCAAAAAATCAGATTTCCAGAAAAATGCTCATCTGCATCTAAATCTGTC
 TTCTTAGGATTTCAGAACTCTTCTCATTATGAAGAAGGTAGCCTGCCCATCTTAAACACAC
 AAACTGACATTTGTTTTTACCAATGGACACAAATTTCTGGGTTCTTTTGCCTGATGGAATCA
 AGACTTCAAAAAATATTAGAAATGACAAATATAGATGGCAAAAGCCAAATTTGTAAGTTATGAA
 ATGCAACGAAATCTTAGTTTGAATAATGCTAAGACATCGGTTCTATTGCTTAATAAGTTGA
 TTTTACTCTGGACGACGTTTCTTCTTATCTTACAAATTTGTTGGCATACATCAGTGGAACT
 TTCAGATCCGAAATGTGACTTTTGGTGGTAAGGCTTATCTTGACCACAAATTCATTTGACTAC
 TCAGATACTGTAATGAGACATATAAATTTGGAGCATGTACATTTTCAGAGTGTTTTACATTCA
 ACAGGATAAATCTATTGCTTTTGACCAAAATGGACATAGAAAACCTGACAATATCAAAATG
 CACAAATGCCACACATGCTTTTCCCGAATTTCTCTAGAAATTTCAATATTAAATTTTGGC
 AATAATATCTTAAACAGACGAGTTGTTTAAAGAACTATCCAATGCCCTCACTTGAAAACCT
 CATTTTGAATGGCATAAAGCTGGAGACCTTTCTTAGTAAGTCTGTTGCTAACACACAC
 CCTTGGAACTCTGGATCTGAGTCAAAATCTATTACAACTAAAAATGATGAAATTTGCTCA
 TGGCCGAAACTGPGCTCAATATGAATCTGTATACATAAATTTGCTGATTCTGTTCTCAG
 GIGCTTGGCCAAAGATTTCAAACTCTGACCTAAATTAATACCAAAATCAAACTGTACCTA
 AAGAGACTATTCTATCTGATGGCTTTACGAGAATTAATATTGCATTTTAAATTTTCTAAGTAT
 CTCCTCGATGCACTCATTTAGTAGACTTTCAGTTCTGAACATTGAAATGAATCTTATTTCT
 CAGCCCATCTCTGGATTTTGTTCAGAGCTGCCAGGAAGTTAAATCTTAAATGCGGGAAGAA
 ATCCATTCGGGTGTAACCTGTGAATTAATAAATTTTCAATCAGCTTGAAACATATTGAGAGGT
 ATGATGTTGATGATGCTCAGATTTCATACCTGTGAATACCTTTAAACCTAAGGGGAACATG
 GTTAAAGAGCTTCTATCTCCAGCAATATCTTGAACACAGCTCTGTTGATTGTCCACATTTG
 TGCTTATATGATGCTTCTGGGTTTGGCTGTGGCTTCTGCTGCTCCACTTTGATCTGCC
 TGGTATCTCAGGATCTAGGTCAATGCACACAACATGGCACAGGTTTAGGAAAACAAACCCA
 AGAACAACTCAAGAGAAATGTCAGATTCCAGCATTTTATTTATACAGTGAACATGATTTCT
 TGTGGGTGAAGAATGAAATGATCCCCAATCTAGAGAAGGAAGATGTTCTATCTTGATTTGC
 CTTTATGAAAGCTACTTTGACCTGGCAAGCATTAGTGAAATATGCTAAGCTTCATTGA
 GAAAGATCATAGTCCATCTTTGTTTGTCTCCCACTTTGTCCAGAATGAGTGGTGCCATT
 ATGAATCTTACTTTTGGCCACCACAATCTCTTCCATGAAATTTCTGATCATATAATCTTATC
 TTAAGTGAACCCATTTCCATTTCTATGCAATTTCCACCAGGATCATATAACTGAAAGCTCTCT
 GGAATAAAAGACATCTTGAATGGCCCAAGGATAGGCGTAATGTGGGCTTTTCTGGGCA
 ACCTTCAGCTGCTATTATGATGTTAATGATATAGCCACAGAGAAATGATGAATGATGAGCA
 TTACAGAGTTAATGAAGAGCTCTCGAGGTTCTACAATCTCTGATGAGAACAGATTTGTCT
 ATAAATTTCCACAGTCCCTGGGAAGTTGGGGACCACATACACTGTTGGGATGTACATTTGATA
 CAACTTTTATGATGGAATTTGACAATATTTATTAATAAATAAAATGGTTATTTCCCTCATATA
 TCAGTTTCTAGAAGGATTTCTAAGAATGATCCTATAGAAAACACCTTCAAGATTTTATAAGG
 GCTTATGGAAGAGGTTTCTATCCAGGATTTGTTTATATCATGAAAATGTGGCCAGGTGCG
 AGTGGCTCAGCTTTGTAATCCCAGCATATGGGAGGCCAAGGTGGGTGACCCACGAGGTCAA
 GAGATGGAGACCATCTGGCCAACTGGTGAACCCCTGTCTCTACTAAAAATGAGGATTTGATA
 GCTTGGGCTGATGGTGCAGCCTGTAGTCCAGCTACTTGGGAGGCTGAGGCAGGAGATCG
 CTGGAACCCGGGAGGTGGCAGTTGCACTGAGCTGAGATCGAGCCATGAGCTCCAGCTGGT
 GACAGAGCGGAGCTCCATCTCAAAAAAAGAAAAAAGAAAAAATGAAAACATCC
 TCATGGCCACAAAATAAGGCTTAATCAATAAATATATAGTACATTAATGTAATATAATTA
 CATGCCACTAAAAAGATAAGGTAGCTGATATTTTCTGGTATGAAAAAATATTAATATTA
 GTTATAAACTATTAGTGGTGGTGAACAACTAATTTGGGTTTGGCAATGAAATGGCATTGA
 ATAAAGGTGAAGAAATCTATACCAGATGTAGTAACAGTGGTTTGGGCTGGGAGTTGGA
 TTACAGGAGGACATTTGATTTCTATGTTGTGATTTCTATAATGTTTGAATTTGTTAGATGA
 ATCTGTATTTCTTTTATAAGTAGAAAAAATAAGATAGTTTTCACAGCCT

FIGURE 34

MRLIRNIYIFCSI VMTAEGDAPELPEERELMTNCSNMSLRKVPADLTPATTTLDLSYNLLFQ
LQSSDFHSVSKLRVLILCHNRIQQLDLKTFFFNKELRYLDLSNNRLKSVTWYLLAGLRYLDL
SFNDFDTPICEEAGNMSHLEILGLSGAKIQKSDFOKIAHLHLNTVFLGFRTLPHYEEGSLP
ILNTTKLHIVLPMDTNFWVLLRDGIKTSKILEMTNIDGKSQFVSYEMQRNLSLENAKTSVLL
LNKVDLLWDDLFLILQFVWHTSVEHFQIRNVTFGGKAYLDHNSFDYSNTVMRTIKLEHVHFR
VFYIQQDKIYLLLT KMDIENLTISNAQMPHMLFPNYPTKFQYLN FANNILTDELFKRTIQLP
HLKTLILNGNKLETL SLVSCFANNTPLEHLDLSQNL LQHKN DENC SWPETVVNMNLSYNKLS
DSVFRCLPKSIQILD LNNNQIQTVPKETIHLMALRELNIAFNFLTDLP GC SHFSRLSVLNIE
MNFILSPSLDFVQSCQEVKTLNAGRNPFRCTCELKNFIQLETYSEVMMVGWSDSYTCEYPLN
LRGTRLKDVHLHELSCNTALLIVTIVVIMVLGLAVAFCCCLHFDLPWYLRMLGQCTQTWHRV
RKTTQEQLKRNVRFHAFISYSEHDSLWVKNELIPNLEKEDGSILICLYESYFDPGKSISENI
VSFIEKSYKSI FVLSPNFVQNEWCHYEFYFAHNL FHENS DHIILILLEPIPFYCIPTRYHK
LKALLEKKAYLEWPKDRRKGLFWANLRAAINVNVLATREMYELQTFTELNEESRGSTISLM
RTDCL

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[illegible]

FIGURE 36

MSRPGTATPALALVLLAVTLAGVGAQGALEDPDYYGQEIWSREPYARPEPELETFSPLP
AGPGEEWERRPQEPRPPKRATKPKKAPKREKSAPEPPPGKHSNKKVMRTKSSEKAANDDHS
VRVAREDVRESCPLGLETLKITDFQLHASTVKRYGLGAHRGRLLNIQAGINENDFYDGAWCA
GRNDLQQWIEVDARRLTRFTGVITQGRNSLWLSDWVTSYKVMVSNDSTWVTVKNGSGDMIF
EGNSEKEIPVLNELPVPMVARYIRINPQSWFDNGSICMRMEILGCPLDPNYYHRRNEMTT
TDDLDFKHNYKEMRQLMKVVNEMCPNITRIYNIGKSHQGLKLYAVEISDHGGEHVGEPEF
HYIAGAHGNEVLGRELLLLLVQFVCQEYLARNARIVHLVEETRIHVLPSLNPDGYEKAYEGG
SELGGWSLGRWTHDGIDINNNFPDLNTLLWEAEDRQNVPRKVPNHYIAIPEWFLSENATVAA
ETRAVIAWMEKIPFVLGGNLQGGELVVAYPYDLVRS PWKTEHTPTDDHVFRWLAYSYST
HRLMTDARRRVCHTEDFQKEEGTVNGASWHTVAGSLNDFSYLHTNCFELSIYVGCDKYPHES
QLPEEWENNRESLIVFMEQVHRGIKGLVRDSHGKGIPNAIISVEGINHDIRTANDGDYWRLL
NPGEYVVTAKAEGFTASTKNCMVG YDMGATRCDFTL SKTNMARIREIMEKFGKQPVSLPARR
LKLGRGRRRQRG

FIGURE 37

CTAAGAGGACAAGATGAGGCCGCCGCCCTCTCATTTCTCCTTAGCCCTTCTGTTCTCCTTGCCCAAGCTGCAGGGG
 ATTTTGGGGAGTGTGGGAGCTCCAAATCCCGGCCCGGCTTCAGCTCTTTCCAGGTGTGTACTCCAGCTCCAGC
 TTCAGCTCCAGCTCCAGGTCCGGCTCCAGCTCCAGCCGACGTTAGGCAGCGGAGGTTCTGTGTCAGGTTGTT
 TTCCAATTTACACGGCTCCGTGGATGACCGTGGGACCTGCAGTGTCTGTTTCCCTGCCAGACACCACTTTTAA
 CCGTGGACAGGTGCAGCGCTTGAATTACAGCTCATGTTCTTCTCAGAAATTGAGAAAGAACTTTCTAAA
 GTGAGGGAATATGTCCAATTAATTAGTGTGTATGAAAAGAACTGTTAAACCTAACTGTCCGAATTGACATCAT
 GGAGAAGGATACCAATTTCTTACACTGAACCTGACCTTCAGCTGATCAAGGTAGAAGTGAAGGAGATGGAAAAAC
 TGGCTCATACAGCTGAAGGAGAGTTTGGTGGAAAGCTCAGAAATTTGTACACAGCTGGAGGTGGAGATAGAAT
 ATGACTCTCTTGGTAGAGAAGCTTGAGACATAGACAAAAACAATGTCCTTGCCATTCCGCCAGAAATCGTGGC
 TCTGAAGACCAAGCTGAAGAGTGTGAGGCTCTAAAGATCAAAACACCCCTGTGTCGCCACCTCTCCCACTC
 CAGGGAGCTGTGGTCATGTTGGTGGTGAACATCAGCAACCCGTGTGTGGTTCAGCTCAACTGTGAGAGGGTT
 TCTTATCTATATGGTCTGGGGTAGGGATTACTCTCCCGAGCATCCAACAAAGGACTGTATTGGGTGGCGCC
 ATTGAATACAGATGGGAGACTGTTGGAGTATTATAGACTGTACAACACACTGGATGATTGCTATTGTATATAA
 ATGCTCGAGAGTTGCCGATCACCTATGGCCAAGTAGTGTACAGCAGTTTACAACAACAACATGTACGTCAAC
 ATGTACAACACCGGGAATATTGCCAGATTAACTGACCACCAACACGATTGCTGTGACTCAAACCTCTCCCTAA
 TGCTGCCTATAATAACCGCTTTTCATATGCTAATGTTGCTTGGCAAGATATTGACTTTGCTGTGGATGAGAATG
 GATTGTGGGTATTATTATCAACTGAAGCCAGCACTGGTAACATGGTGATTAGTAACTCAATGACACCACTT
 CAGGTGCTAAACACTTGGTATACCAAGCAGTATAAACCATCTGCTTCAACGCCCTTCATGGTATGTGGGTCT
 GTATGCCACCCGTAATGAACACCAGAACAGAGAGATTTTTTACTATTATGACACAACACAGGGAAGAGG
 GCAAACTAGACATTGTAATGCATAAGATGCAGGAAAAAGTGCAGAGCATTAACTATAACCCCTTTTGACCAGAAA
 CTTTATGTCTATAACGATGGTTACCTTCTGAATTATGATCTTTCTGCTTGCAGAAAGCCCCAGTAAAGCTGTTTA
 GGAGTTAGGGTGAAAGAGAAAAATGTTTGTGAAAAAATAGTCTTCTCCACTTACTTAGATATCTGCAGGGGTGT
 CTAAGAAGTGTGTTCAATTTGCAGCAATGTTTAGGTGCATAGTTCTACCACACTAGAGATCTAGGACATTTGTCT
 TGATTTGGTGAATTCTCTTGGGAATCATCTGCCCTTCAGGCGCATTTTGCAATAAAGTCTGCTAGGTTGGGA
 TTGTCAGAGGTCTAGGGGCACCTGTGGGCTAGTGAAGCCTACTGTGAGGAGGCTTCACTAGAGGCTTAAATTA
 GGAATTAAGGAACCTAAACCTCAGTATGGCGTCTAGGGATTCTTTGACAGGAAATATTGCCAATGACTAGTC
 CTCATCCATGTAGCACCACCTAATTTCTCCATGCCGTGAAGAAACCTGGGACCTTAGTTAGGTAGATTAATATCT
 GGAGCTCCTCGAGGGACCAAACTCCCAACTTTTTTTTCCCTCACTAGCACCTGGAATGATGCTTTGTATGTGG
 CAGATAAGTAATTTGGCATGCTTATATATTCTACATCTGTAAGTGTCTGAGTTTATGGAGAGAGCCCTTTT
 ATGCATTAATTTGTACATGGCAATAAATCCAGAAGGATCTGTAGATGAGGCACCTGCTTTTTCTTTTCTCTC
 ATTGTCACCTTACTAAAAGTCAGTGAATCTTACCTCATAACTTCTTCCAAAGGCAGCTCAGAAGATTAG
 AACCAGACTTACTAACCATTCCACCCCCACCAACCCCTTCTACTGCTACTTTAAAAAATTAATAGTTTT
 CTATGGAATGATCTAAGATTAGAAAAATTAATTTCTTTAATTTCAATTATGACTTTTATTTACATGACTCTA
 AGACTATAAGAAATCTGATGGCAGTGAACAAGTGTCAATTTATGTTATCTAATAAAGACCTTGGAGCAT
 TGTGCAACTTATGAGTGTATCAGTGTGTCATGTAATTTTGGCTTTGTTTAAAGCTGGAACTGTAGAAAAAT
 GAAAAATTAATTTTTTTTTCTAGGACGAGCTATAGAAAAAGCTATTGAGATGATCTAGTAACTGACAGTGT
 TGCAAACTTGTCTGGTGTATGTGATGTGCTTCTGTGCTTTTGAATGACTTATCATCTAGTCTTTGTCTATTTT
 TCCTTTGATGTTCAAGTCTAGTCTATAGGATTGGCAGTTTTAAATGCTTTACTCCCCCTTTTAAAAATAATGAT
 TAAAATGTGCTTTGAAAAAATAAAAAAAAAAAAAAAAAA

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FIGURE 38

MRPGLSFLLALLFFLGQAAGDLGDVGPPIPSPGFSFPGVDSSSFSSSSRSGSSSSRSLGS
GGSVSQLFSNFTGSVDDRGTCQCSVSLPDTTFFVDRVERLEFTAHVLSQKFEKELSKVREYV
QLISVYEKKLLNLTVRIDIMEKDTISYTELDFELIKVEVKEMEKLVIQLKESFGGSSEIVDQ
LEVEIRNMTLLVEKLETLDKNNVLAIRREIVALKTKLKECEASKDQNTPVVHPPPTPGSCGH
GGVVNISKPSVVQLNWRGFSYLYGAWGRDYSPOHPNKGLYWVAPLNTDGRLLLEYRLYNTLD
DLLLYINARELRITYGQGSQTAVYNNMYVNMNTGNIARVNLTTNTIAVTQTLNAAAYNNR
FSYANVAWQDIDFAVDENGLWVIYSTEASTGNMVISKLNDTTLQVLNTWYTKQYKPSASNAF
MVCGLYATRMTNTRTEEIFYYYDTNTGKEGKLDIVMHKMQEKVQSINYNPFDQKLYVYNDG
YLLNYDLSVLQKPQ

FIGURE 39

GCTCTGAAGACCAAGCTGAAAAGAGTGTGAGGCCTCTAAAGATCAAACACCCCTGTCGTCCAC
CCTCCTCCCACTCCAGGGAGCTGTGGTCATGGTGGTGTGGTGAACATCAGCAAACCGTCTGT
GGTTCAGCTCAACTGGAGAGGGTTTTCTTATCTATATGGTGCTTGGGGTAGGGATTACTCTC
CCCAGCATCCAAACAAAGGNATGTATTGGGNGCGCCATTGAATACAGATGGGAGACTGTTG
GAGTATTATAGACTGTACAACCCACTGGATGATTTGCTATTGTATATAAATGCTCGAGAGTT
GCGGATCACCTATGGCCAAGGTAGTGGTACAGCAGTTTACAACAACAACATGTACGTCAACA
TGTACAACACCGGGNATATTGCCAGAGTTAACCTGACC

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FIGURE 40

TCTCGCAGATAGTAAATAATCTCGGAAAGGCGAGAAAGAAGCTGTCTCCATCTTGTCTGTAT
 CCGCTGCTCTTGTGACGTTGTGGAGATGCGGGGAGCGTCTGGGGCTGTGCTCCATGGCGAGCT
 GGATACCCTGTTTGTGTGAAGTGCCCGGTGTTGCTATGCCGATGCTGCTTCCATGGGAAAC
 AACTCCACTGTAACTAGATGTATCTGCACTTTTCTTGTGTTGGAGTATGTGTAGCTTG
 TCTAATCTTGTATACCAGGAATGGAAGAACAACTGAATAAGATTCTCGGATTTTGTGAGAATG
 AGAAAGTGTTGTCTCTTGTAACTTTTGGTTGGCTATAAAGCTGTATATCGTTTGTGCTTT
 GGTTTGGCTATGTTCTCTCTCTCTCTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGA
 TCTTAGAGCTGCAGTGCACAAATGGATTTTGGTCTTTAAATTTGCTGCAGCAATTGCAAATTA
 TTATTGGGCGATTCTCATTTCCAGAAGGAACTTTACAACGTGTGTGTTTATGTAGGCATG
 CGAGGTGCGCTTTTGTTCATCTCATACAACCTAGTCTTACTTATTGATTTGCACATTCATG
 GCATGAATCCGTGGTTGAAAAAATGGAAGAAGGGAACCTCGAGATGTGGTATGCAGCCTTGT
 TATCAGCTACAGCTCTGAATTATCTGCTGTCTTTAGTTGCTATCGTCTGTCTTTGTCTAC
 TACACTCATCCAGCCAGTTGTTCCAGAAAACAGGCGTTTCATCAGTGTCAACATGCTCCTCTG
 CGTTGGTGCTCTGTGAATGCTATATCTGCAAAAATCCAAGAATCACAACCAAGATCTGGTT
 TGTACAGTCTTTCAGTAATTACAGTCTACACAATGTATTTGACATGGTCAGCTATGACCAAT
 GAACCCGAAACAAATTGCACCCAAAGTCTACTAAGCAATAATTTGGCTACAATACAACAGCAC
 GTGCCCAAGGAAGGGCAGTCAGTCCAGTGGTGGCATGCTCAAGGAATTATAGGACTAATTC
 TCTTTTGTGTGTGATTTTATCCAGCATCCGTACTTCAAACAATAGCTCAGGTATAATAA
 CTGACCTTAAACAAGTCATGAATCTACATTAATAGAAGATGGTGGAGCTAGAGATGATGGATC
 ACTGGAGGATGGGACAGTGTTCACCGAGCTGTAGATAATGAAAGGATGGTGTCACTTACA
 GTTATTGCTCTTCCACTTCACTGCTTTTCTGGCTTCACTTTATATCATGATGACCCTTACC
 AACTGGTCCAGGTATGAACCCCTCTCGTGAGATGAAAGTCAGTGGACAGCTGTCTGGGTGAA
 AAATCTCTTCCAGTTGGATGGCATCGTGTGTATGTTTGGACACTCGTGGCACCCTTGTGTC
 TTACAAATCGTGAATTTGACTGAGCTGAGACTTCTAGCATGAAAGTCCCACCTTTGATTATGC
 TTATTTGAAACAGTATTCCCAACTTTGTAAAGTTGTGTATGTTTGTCTGCCATGTAAC
 TTCTCCAGTGTCTGGCATGAATTAGATTTTACTGCTTGTCTATTTTGTATTTTCTTACCAA
 GTGCATTCATGATGTGAAGTGAATGAATTTGCAGAGGAAAGTTTATGAATATGGTGATGAGT
 TAGTATAAGTGGCCATTATTGGGCTTATCTCTGCTCTATAGTTGTGAAATGAAGAGTAAAA
 ACAATTTGTTTGTGACTAATTTAAAAATTATATTAGACCTTAAAGCTGTTTGTAGCAAGCATAAA
 GCAATCTGATGGCTGCTTTTGAATATTTGATGTGTTGCCCTGGCAGGATACTGGCAAAGAAC
 ATGCTTTATTTTAAAAATTTATAACAAGTCACTTAAATGCCAGTTGTCTGAAAAATCTTATA
 AGTGTTTTACCCTTGATACGGAAATTTACACAGGTAGGGAGTGTATTAGTGGACAAATAGTGTAGG
 TTATGGATGGAGGTGTGCGTACTAAATTTGAATAACGAGTAAATAATCTTACTTGGGTAGAGA
 TGGCCTTTGCCAACAAAGTGAAGTGTGTTTGGTTGTTTAAACTCATGAAGTATGGGTTGAGT
 GGAATGTTTGGAACTCTGAAGGATTTAGACAAGGTTTGGAAAGGATAATCATGGGTTAGA
 AGGAAGTGTGTTGAAAGTCACTTGAAGTTAGTTTGGGCCAGCAGCGTAGCTCACCCCT
 GGTAAATCCAGCACTTTGGGAGCTTAAAGTGGGTAGATTACTTGAGCCAGGAATTCAGACCA
 GCTTGGCACATGGTGAACCTGTTCTATAAAAAATATCTGGCTTTGAGCATATGCCTGTGGTC
 CAGCATGAGAGGCTAGTGAAGATTTGCTGAGCCGAGAGCCAAAGGTTGCACTGAGCAAGTCA
 CGTCACTGCACCTGACTGGCAGAGAGTAAGCCAAAAAATATATATATTGAAATCAAGG
 AGGCAAAATTTGACAGGGAAGGAAGTAACTGCAAAACCACTAGGCTTTAGTAGGTACTTAT
 ATAAACTCTAGTCCAGTTCTCTCATTTAAAAAAATGAAGACACTGAAATACAGACTTAAATA
 GCTCAGATAGCTAATTTAGGAATTTCAAGTTGGCCAATAATAGCATTTCTCTGTACATTTAA
 AAATATTTCTATTCAAAATACATGCATATTGATTTACACCTCATACTGTGATAAATTAATGT
 CATGTGGATTGCTGGTGTCCAGCATGACCCATAAGAGGTGAGAAGAATGATGGAATGTTTT
 AGAATAAACCCTGCTTATAGTATACTACACAGTTCAAAGAGTGTTTAAATGCTTTTGTAT
 TTACTGGCATGTAAATGAAATATATAGATTATTGTAACCTTTCAACCTGAAATCAAGCAGT
 ATGAGAGTTTAAATTTTGTATGTGCTACTAGTGTCTAATGAAGCTTTTAAATCTCAACT
 TCTCTTTTAAATATTTAATGTGAATGAATAACAATTCAGCTTAATCCCCAAC
 TTATCTGTGTGTAGACATTGTATCCCAATTTTGAATGGCTGTGTTTTACCTCTAAATAA
 ATGAATTCAGAGAAAAA

FIGURE 41

MGSVLGLCSMASWIPCLCGSAPCLLRCCPCSGNNSTVTRLIYALFLLVGVCVACVMLIPGME
 EQLNKIPGFCENEGVVPNCILVGKYAVYRLCFLGLAMFYLLSLMIKVKSSSDPRAAVHNG
 FWFFKFAAAIAIIIGAFFTPEGFTTWWVFVGMAGAFCLILQLVLLIDFAHSWNESWVEKM
 EEGNSRCWYAALLSATALNYLLSLVAIVLFFVYYTHPASCSENKAFISVNMLLCVGASVMSI
 LPKIQESQPRSGLLQSSVITVYTMYLTSWAMTNEPETNCNPSLLSIIGYNTTSTVPKEGQSV
 QWWHAQGIIGLILFLLCVFYSIIRTSNNSQVNKLTLTSDSTLIEDGGARSDGSLEDGDDVH
 RAVDENRDGVTYSYSFFHFMLFLASLYIMMTLTNWSRYEPSREMKSQWTAVVWPKISSWIGI
 LLYVWTLVAPVLTNRDFD

FIGURE 42

GCGAGAAAGAAGCTGTCTCCATCTTGTCTGTATCCCGCTGCTTCTTNGACGTTGTGGAGAT
GGGGAGCGTCCCTGGGGCTGTGCTCCATGGCGAGCTGGATACCATGTTTGTGTGGAAGTGCC
CCGTGTTTGCTATGCCGATGCTGTCCTAGTGGAAACAANTCCACTGTAAGTATGATTGATCTA
TGCACTTTTCTTGCTTGTGGAGTATGTGTAGCTTGTGTAATGTTGATACCAGGAATGGAAG
AACAACGAATAAGATTCTCTGGATTTTGTGAGAATGAGAAAGGTGTTGTCCCTTGTAACATT
TTGGTTGGCTATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTTCT
CTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGAT
TTTGGTTCTTTAAATTGCTGCAGCAATTGCAATTATTATTGGGGC

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FIGURE 43

GTTATTGTGAACTTTGTGGAGATGGGAGGTCNTGGGGCTGTGTTCCATGGCGAGCTGGATAC
CANGTTTGTGTGGAAGTGCCCGTGTTTGNATGCCGATGCTGTCCTAGTGGAAACAANTCC
ACTGTAATTAGATTGATNTATGCACTTTTNTTGCTTGTGGAGTANGTGTAGCTTGTGTAAT
GTTGATACCAGGAATGGAAGAACAACCTGAATAAGATTCTGGATTTTGTGAGAATGAGAAAG
GTGTTGTCCCTTGTAAACATTTGGTTGGCTATAAAGCTGTATATNGTTTGTGCTTTGGTTTG
GCTANGTTCTATNTTCTTCTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAG
AGCTGCAGTGACAAATGGATTTTGGTTTTTTAAATTTGCTGCAGCAATTGCAATTATTATTG
GGGC

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FIGURE 44

AAGAAGCTGTCTCCATCTTGTCTGTATCCGCTGCTCTTGTGAACGTTNTGGAGATGGGGAGC
GTCCTTGGGGTTGTGCTCCATGGCGAGCTGGATACCATGTTTGTGTGGAAGTGCCCCGTGTT
TGCTATGCCGATGCTGTCTAGTGGAACAACCTCCACTGTAACTAGATTGATCTATGCACTT
TTCTTGCTTGTTGGAGTATGTGTAGCTTGTGTAATGTTGATACCAGGAATGGAAGAACAAC
GAATAAGATTCCCTGGATTTTGTGAGAATGAGAAAGGTGTTGCCCTTGTAACATTTTGGTTG
GCTATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTTCTCTTTTA
CTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGATTTTGGTT
CTTTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGC

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FIGURE 45

GCTGTCCTTAGTGGAAACAANTCCAACCTTGTAACCTGGATTGATCTATGCACCTTTTCCTTG
CTTGTTGGAGTATGTGTAGCTTTGTGTAATGTTGTTCCAGGATTGGANGAACAACTGAATA
AGATTCCCTGGATTTTTGTGAGAATGAGAAAGGTGTTGTCCCCTTGTAACATTTTTGGTTGGC
TATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTCTCTTTACT
AATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGATTTTTGGTTCT
TTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGCATTCTTCATTCCAGAAGGAACTTTT
ACAACTGTGTGGTTTTATGTAGGCATGGCAGGTGCCTTTTGTTTCATCCTCATACAAC TAGT
CTTACTTATTGATTTTGACATT CATGGAATGAATCGTGGGTTGAAAAATGGAAGAAGGGA
ACTCGAGATGTTGGTATGCAGCCTTGTTATCAGCTACAGCTCTGAATTATCTGCTGTCTTTA
GTTGCTATCGTCCTGTTCTTTGTCTACTACACTCATCCAGCCAGTTGTTTCAGAAAACAAGGC
GTTTCATCAGTGTCAACATGCTCCTCTGCGTTGGTGCTTCTGTAATG

FIGURE 46

CTCGGGCGCGCAGGCGAGCTCGGTTTGCCTTGCATTGAGCTGCGGGTCGCGCGCGCGCGGCTCTCCAAT
GGCAAAATGTGTGTGGCTGAGGCGAGCGCGAGGCTTTCGGCAAAAGCAGTGCAGTGTTCGACAGCCGGGCGGAG
TCCGTGAAAGAGCAGATAAAAGAAACATTATTAACTGTGATTACGAGGAGCGCGCGCGGGGCTGTGCG
ACTCCCGCGGCAACATTTGGCTCCCTCCAGCTCCGAGAGGAGGAGAAGAGAAGCGGAAAGAGGCAAGATTCAC
GTCTGTTTTCAGCAAAATGGAACCTGATCGATGGCCCTCCTGAATTTATCAGATATTTGATTATTAGCGATGCC
CCCTGGTTTGTGTGTTACGACACACACGTGCAACAGGCTGTGGCTCGCTTCCCTCCCTCGTTTCAGCTGT
TGGGCGAATCCCACATCTCTGTTTCACTCTCCGCGAGGGCGAGCAGGAGAGTGTGCCAATCTCGGAGTGG
AAGAGGGACGAGGGAAAAAGAAACAAGCCACAGACGCAACTTGAGACTCCGCGATCCCAAAAGAACACAGAT
CAGCAAAAAAGAGAGTGGGCGCCCGGAGGCTTGTGCTGTCTGCTGTCGCCCACTGTGTTCCCTGTCTGGG
TGAAGCTCGGCTTCTGTGCGACCCACCGCTGAAAGCAGGTTTCAGAGGACCCGAGGAACATCCGCCCA
ACATCATCTGTTGCTGACGGACGACGAGGATGGAGCTGGGTCCATGCGAGTGATGAACAAGACCCGCGG
ATCATGGAGCAGGCGGGGGCGCACTTCATCAACGCTTGTGACCAACCCATGTGCTGCCCTCACGCTCTCT
CATCTCTACTGGCAAGTACGTCACAAACCAACACCTACACCAACATGAGAAGTGTCTCTCGCTCTCTGGC
AGGCACAGCAGAGAGCCGCACTTTGCGGTGTACTCAATAGCACTGGCTACCGGACAGCTTTCTTCGGGAAG
TATCTTAATGAATCAACGCTCTACGTGCCACCGGCTGGAGGAGTGGGTCCGACTCTTAAAACTCCG
CTTTTATACTACACGCTGTGTCGGAACGGGTTGAAAGAGAGCAGGCTCCGACTCTCAAGGATTACCTCA
CAGACCTCATCAACCAATGACAGCGTGAGCTTCTTCGCGAGTCCAAGAAGATGTACCCGACAGGCGAGTCTCT
ATGGTCATCGCCATGCGAGCCGCCCGGCTGAGGATTTCAGCCCAACAATTTACGGCTCTTCCCAACGCG
ATCTCAGCAGCATCAGCCGAGCTACAACTACGCGCCCAACCCGAGACAACTGGATCATGGCTACACGGGG
CCATGAGGCCCATTCACATGGAATTCACCAACATGCTCAGCGGAAGCGCTTGCAGACCTCATGTTCGGTGGAC
GACTCCATGGAGACGATTACAACATGCTGGTTGAGAGCGGCGAGCTGGACAAACAGTACATCGTATACACCGG
CGACAGACGTTCCACATCGGGCAGTTTGGCTGGTGAAGGAAATCCATGCCATATGAGTTGACATCAGG
TCCGGTTCTAGTGGAGGGGCCCAACGCTGGAAGCGGCTGTCTGAATCCCACTCGTCCATCAACATGACCTT
GCCGCCACCTCTGGACATTCAGGCTTGGACATACCTGCGGATATGGACGGGAAATCCATCTCAAGCTGT
GGACAGCGGCGCGGCGGTGAATCGGTTTCACTTGAAGAAGAGATGAGGCTTGGCGGGACTCCTCTTGTGTG
AGAGAGGCAAGCTGTACACAAGAGAGACATGACAAGGTGGAGCCCGAGGAGGAACTTCTGCCCAAGTAC
CAGCGCTGAAGGACCTTGTTCAGCGTGTGAGTACGAGCGGCGTGTGAGCAGCTGGGACGAAGTGGCAGT
TGTGGAGGACGCCAGGGGAAGCTGAAGCTGCATAAGTGCAGGGGCCCATGCGGCTGGGCGCGACGAGCC
TCTCCACCTCTGCGCCAACTACTACGGGCGAGGCGAGGCTGCACTGTGACAGCGGGGACATCAAGCT
AGCTTGCCGGGACGCCGGAAGAACTTCAAGAAGAAGTACAAGGCCAGTATGTCCGCACTCGCTCCATCG
CTCAGTGGCCATCGAGGTGACGCGGAGGTGTACACGCTAGGCTGGGTGTGCGCGCCGAGCCCGAACTCA
CCAAGCGGCACTGGCAGCGGCCCTGAGGACCAAGATGACAAGGATGGTGGGACTTCAGTGGCACTGGAGG
CTTCCCGACTACTCAGCGGCCAACCCCATTAAGTGAACATCGTGCTACATCTAGAGAAGCAGACGATCA
GTGTGACCTGGACCTGTACAGCTCCCTGAGGCTTGAAGAAGCACAAGCTGCACATGCACACAGAGTGA
CCCTCGAGAACAATTAAGAACTGAGGGAAGTCGAGGCTCACTGAAGAAAGCGGGCCAGAGAATGTGAC
TGTCAAAATCAGCTACCAACCCGACCAAGGCGCCCTCAAGCACAGAGGCTCAGTCTGCATCTTTTCAG
GAAGGGCTCGAAGAGAAGGACAGGTTGGGCTGTTGCGGAGCAGAGCGCAAGAAGAACTCCGAGGCTG
TCAAGCGCTTCGAGAACAACGACGCTGAGCAGTGCAGGCTTCACTGCTTCAACCGACCAACAGCAGTGG
CAGAGCGCGCTTTTCGAGCACTGGGGCTTTCTGTGCTCGACGAGCCCAACATACACGATCTGCTGAT
GAGGACCATCAATGAGACTCACAATTTCTCTTCTGTGAATTTGAACCTGGCTTCTAGAGTCTTGTATCTCA
ACACAGCACTTACAGCTGATGAATGCAAGTGAACACACTGGACAGGAGTGTCTCAACGACTACAGCTACAG
CTCATGGAGCTGAGGAGCTGCAAGGGTTACAAGCAGTTAACCCCGGAGCTGGAACATGAGCTGGATGGAG
AAGCTATGACCAATACAGGAGTTTACGCTGGAAGTGGCAGAAATGAAGAGCTCTTCCAATCACTGG
GACAACTTGGGAGGCTGGGAAGTTTGAAGAAACAAGAGTGGAGCTCAAAAAGATAGAGGATCACTGSA
CTGCAGGCAATGAAACACATGTGGTGATTTCAGAGCACTGTGCTATTGGCCAGGAGGCTGAGAAAG
ARGCAGCAGCTTCAGTCAACATCAGAGATTCTGGAGGATTAACGACGAGGACAGAGATACTTCAGGAAGTCC
ATTTTTCCTGCTTTTGGTTTGGATTATACCTCAGCAGTGCACAAATGCAATTTTGTGTAAGAAGT
ACCACTAACCTCCCGAGAGCTCACAAGGAAACGAGGAGGACGAGCGAGAGAGATTTCTTGGAAATTC
TCCCAAGGGCGAAGCTTATGGAATTTTAAATCATAGGGGAAAGCAGCTGTGTTCTTAAATCTCTTATTTCT
TGTGGTTTGTACAAGAAGGAACTAAGAAGCAGGACAGAGGCAACGTTGGAGGCTGAAACAGCTGCAGAGG
TTTGACATGAGTCAAGCACAAGAGAGATGACATTTTACCTAGCACTATAAACCCCTGGTTGCCCTGAAGAA
CTGCTTATTGTATATATGTGACTATTTACATGTAATCAACATGGGAACTTTTAGGGGAACTATAAGAATA
CCCAATTTTCAGAGTGGTGGTGTCAATAAACGCTTGTGGCCAGTGAAGAAGAA

FIGURE 47

MGPPSLVLCILSATVFSLLGGSSAFLSHHRLKGRFQRDRRNIRPNIIILVLTDDQDVELGSMQ
VMNKTRRIMEQGGAHFINAFVTPMCCPSRSSILTGKYVHNHNTYTNNENCSSPSWQAQHE
RTFAVYLNSTGYRTAFFGKYLNEYNGSYVPPGWKEWGLLKNSRFYNYTLCRNGVKEKHGSD
YSKDYLTDLITNDSVSFFRTSKKMYPHRPVLMVISHAAPHGPEDSAPQYSRLFNPASQHITP
SYNYAPNPDKHWIMRYTGPMKPIHMEFTNMLQRKRLQTLMSVDDSMETIYNMLVETGELDNT
YIVYTADHGHIHQFGLVKGKSMPEFDIRVFPFYVRGPNVEAGCLNPHIVLNIDLAPTILDI
AGLDIPADMDGKSILKLLDTERPVNRFHLKKKMRVWRDSFLVERGKLLHHRDNDKVDAAQEN
FLPKYQVRKDLQRAEYQTACEQLGQKWQCVEDATGKLLHKCKGPMRLGGSRALSNLVPKY
YGGSEACTCDSDYKLSLAGRRKKLFKKKYKASYVRSRSIRSAIEVDGRVYHVGLGDAQ
PRNLTKRHWPGAPEDQDDKDGDFSGTGGLPDYSAANPIKVTHRCYILENDTVQCDLDLYKS
LQAWKDKHLHIDHEIETLQNKIKNLREVRGHLKKRPEECDCHKISYHTQHKGRLKHRGSSL
HPFRKGLQEKDKVLLREQKRKKLRKLLKRLQNNDTCSMPGLTCFTHDNQHWQTAPFWTLG
PFCACTSANNNTYWCMRTINETHNLFCEFATGFLEYFDLNTDPYQLMNAVNTLDRDVLNQL
HVQIMELRSCKGYKQCNPRTRNMDLDGGSYEQYRQFQRRKWPEMKRPSSKSLGQLWEGWEG

FIGURE 48

AACAAAGTTCAGTGACTGAGAGGGCTGAGCGGAGGCTGCTGAAGGGGAGAAAGGAGTGAGGA
GCTGCTGGGCAGAGAGGGACTGTCCGGCTCCCAGATGCTGGGCCCTCCTGGGGAGCACAGCCC
TCGTGGGATGGATCACAGGTGCTGCTGTGGCGGTCTCTGCTGCTGCTGCTGCTGCTGGCCACC
TGCCCTTTTCCACGGACGGCAGGACTGTGACGTGGAGAGGAACCGTACAGCTGCAGGGGGAAA
CCGAGTCCGCCGGGCCAGCCTTGCCCTTCCGGCGCGGGGCCACCTGGGAATCTTTACCC
ATCACCGTCATCCTGGCCACGTATCTCATGTGCCGAATGTGGCCCTCCACCACCACCACCAC
CCCCGCCACACCCCTCACCACTCCACCACCACCACCACCCCCACCGCCACCATCCCCGCCA
CGCTCGCTGAAGGCTGCTGTGCGCCGGTGCCCTGTGGACAGCAGCTGCCCTGCCCTCCCATCTG
TTCCCAGGACAAGTGGAACCCCATGTTCCATGTGGAAGGATGCATCTCTGGGGTGAACGAGG
GGAACAATAGACTGGGGCTTGCTCCAGCTGCATTGTCATGGCATGCCCCAGTGTACTATGGC
AGCAGAGAATGGAGGAACACTGGGTCTGCAGTGTGAAGGTTTGGGGAGTGGAGAGCAAGG
GTGCTCTTTGGGGCTGGACAGCCCGTCTTGTGACAGTGACTCCCAGTGAGCCCCAGAAATG
ACAAGCGTGTCTTGGCAGAGCCAGCACACAAGTGGATGTGAAGTGCCCGTCTTGACCTCCTC
ATCAGGCTGCTGCAGGCCCTCTGGCGGGCAGGGCACTGGGAGAGGCCCTGAGAAATGCTCTTTT
GGTTTGAGAAGGCAGTGTGAGGCTGCACAGTCAATTTCATCGGTGCCTTAGTCCAAGAAAAT
AAAAACCACTAAGAAGCTTTAAAAAAAAAAAAAAAAAAAAA

FIGURE 49

MLGLLGSTALVGWITGA AVAVLLLLLLLATCLFHGRQDCDVERNRTAAGGNRVRAQWPFR
RRGHLGIFHHHRHPGHVSHVPNVGLHHHHHPRHTPHHLHHHHHPRHHPRHAR

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FIGURE 50

GGCGGCTGCTGAGCTGCCTTGAGGTGAGTGTGGGGATCCAGAGCCATGTCGGACCTGCTA
CTACTGGGCTGATTGGGGGCTGACTCTCTTACTGCTGCTGACGCTGCTGGCCTTTGCCGG
GTACTCAGGGCTACTGGCTGGGGTGGAAGTGAGTGTGGGTACACCCCATCCGCAACGTCA
CTGTGGCCTACAAGTTCCACATGGGGCTCTATGGTGAGACTGGCGGGCTTTTCACTGAGAGC
TGCAGCATCTCTCCAAAGCTCCGCTCCATCGCTGTCTACTATGACAACCCCATCGGTGCC
CCCTGATAAGTGCCGATGTGCCGTGGGCAGCATCCTGAGTGAAGGTGAGGAATCGCCCTCCC
CTGAGCTCATCGACCTCTACCAGAAATTTGGCTTCAAGGTGTTCTCTTCCCGGCACCCAGC
CATGTGGTGACAGCCACCTTCCCCTACACCACCATTTCTGTCCATCTGGCTGGCTACCCGCCG
TGTCATCCTGCCTTGGACACCTACATCAAGGAGCGGAAGCTGTGTGCCATCCTCGGCTGG
AGATCTACCAGGAAGACCAGATCCATTTTATGTGCCCACTGGCACGGCAGGGAGACTTCTAT
GTGCCTGAGATGAAGGAGACAGAGTGGAAATGGCGGGGGCTTGTGGAGGCCATTGACACCCA
GGTGGATGGCACAGGAGCTGACACAATGAGTGACACGAGTTCTGTAAGCTTGAAGTGAGCC
CTGGCAGCCGGGAGACTTCAGCTGCCACACTGTACCTGGGGCGAGCAGCCGTGGCTGGGAT
GACGGTGACACCCGACGCGAGCACAGCTACAGCGAGTCAGGTGCCAGCGGCTCCTCTTTGA
GGAGCTGGACTTGAGGGCGAGGGGCCCTTAGGGGAGTCACGGCTGGACCCTGGGACTGAGC
CCCTGGGGACTACCAAGTGGCTCTGGGAGCCACTGCCCCTGAGAAGGGCAAGGAGTAACCCC
ATGGCCTGCACCCCTCCTGCAGTGCAGTTGCTGAGGAAGTGAAGAGTCTCCAGCAGACTCT
CCAGCCCTCTTCTCCTTCTCTGGGGGAGGAGGGGTTCTGAGGGACCTGACTTCCCCTGC
TCCAGGCTCTTGTCTAAGCCTTCTCCTCACTGCCCTTTAGGCTCCAGGGCCAGAGGACCA
GGGACTATTTTCTGCACCAAGCCCCAGGGCTGCCGCCCTGTTGTGTCTTTTTTTCAGACTC
ACAGTGGAGCTTCCAGGACCCAGAATAAAGCCAATGATTACTTGTTTACCTGGAAAAAA
AAAAA

MSDLLLLGLIGLTLTLLLLTLLAFAGYSGLLAGVEVSAGSPPIRNVTVAYKFHMGlyGETGR
LFTESCSISPKLRSIAVYDNPMPVDPDKRCVGSILSEGEESPSPELIDLQYKFGFKVFS
FPAPSHVVTATFPYTILSIWLATRVRHPALDITYIKERKLCAYPRLEIYQEDQIHFMCPLAR
QGDFYVPEMKETEWKRWGLVEAIDTQVDGTGADTMSDTSVSVLESPGSRETSAAATLSPGAS
SRGWDDGDRSEHSYSESGASGSSFEELDLEGEGLGESRLDPGTEPLGTTKWLWEPTAPEK
GKE

FIGURE 52

CCGCGGGAACGCTGTCCTGGCTGCCGCCACCCGAACAGCCTGTCCTGGTGCCCCGGCTCCCT
GCCCCGCGCCAGTCA**ATG**ACCCTGCGCCCTCACTCCTCCCGCTCCATCTGCTGCTGCTGCT
GCTGCTCAGTGCGGCGGTGTGCCGGGCTGAGGCTGGGCTCGAAACCGAAAGTCCCGTCCGGA
CCCTCCAAGTGGAGACCTGGTGGAGCCCCAGAACCATGTGCCGAGCCCGCTGCTTTTGGA
GACACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACGTATTATTGACACCTCCCT
GACCAGAGACCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGATTCCAGGTCTGGAGCAGA
GTCTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTCTTCTCACTTGGCCTAT
GGAAAACGGGGATTTCCACCATCTGTCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCT
GATTGCACTAATCCGAGCCAACACTACTGGCTAAAGCTGGTGAAGGGCATTTTGCCTCTGGTAG
GGATGGCCATGGTGCCAGCCCTCCTGGGCCTCATTGGGTATCACCTATACAGAAAGCCAAT
AGACCCAAAGTCTCCAAAAAGAACTCAAGGAAGAGAAACGAAACAAGAGCAAAAAGAA**TA**
ATAAATAATAAATTTTAAAAAACTTAAAAAAAAAAAAAAAAAAAA

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MTLRPSLLPLHLLLLLLLSAAVCRAEAGLETESPVRTLQVETLVEPPEPCAEPAAFGDTLHI
HYTGSLVDGRIIDTSLTRDPLVIELGQKQVIPGLEQSLDMCVGEKRAIIPSHLAYGKRGF
PPSPADAVVQYDVELIALIRANYWLKLVKGILPLVGMAMVPALLGLIGYHLRYKANRPKVS
KKKLKEEKRNSKKK

FIGURE 54

CCCGGGAACGTGTTCTTGCGCTGCCGCACCCGAACAGCCTGTCCTGGTGCCCCGGCTCCCTGC
CCCGCGCCAGTCATGACCCCTGCGCCCCCTCACTCCTCCGCTCCATCTGCTGCTGCTGCTGC
TGCTCAGTGCGGCGGTGTGCCGGCTGAGGCTGGGCTCGAAACCGAAAGTCCCGTCCGGACC
CTCCAAGTGGAGACCCTGGTGGAGCCCCAGAACCATGTGCCGAGCCCGCTGCTTTTGAGA
CACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACGTATTATTGACACCTCCCTGA
CCAGAGACCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGATTCCAGGTCTGGAGCAGAGT
CTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTCTTCTCACTTGGCCTATGG
AAAACGGGGATTTCCACCATCTGTCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCTGA
TTGCACTAATCCGAGCCAACCTACTGGCTAAAGCTGGTGAAGGCATTTTGCCTCTGGTAGGG
ATGGCCATGGTGCCACCCTCCTGGGCCTCATTGGGTATCACCTATACAGAAAGGCCAATAGA
CCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAACAAGAGCAAAAAGAAATAATA
AATAATAAATTTTAAAAAAGCTTA

FIGURE 55

CCGAAAGTCCCGTCCGGACCCCTCCAAGTGGAGACCCTGGTGGAGCCCCCAGAACCATGTGCC
GAGCCCGCTGCTTTTGGAGACACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACG
TATTATTGACACCTCCCTGACCAGAGACCCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGA
TTCCAGGTCTGGAGCAGAGTCTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATT
CCTTCTCACTTGGCCTATGGAAAACGGGGATTTCACCATCTGTCCCAGCGGATGCAGTGGT
GCAGTATGACGTGGAGCTGATTGCACTAATCCGAGCCAACCTACTGGCTAAAGCTGGTGAAGG
GCATTTTGCCCTCTGGTAGGGATGGCCATGGTGCCAGCCCTCCTGGGCCTCATTGGGTATCAC
CTATACAGAAAGGCCAATAGACCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAA
CAAGAGCAAAAAGAAATAATAAATAATAAATTTAAAAAACTTAAAA

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FIGURE 56

CTGCTGCATCCGGGTGTCTGGAGGCTGTGGCCGTTTGTGTTTCTTGGCTAAAAATCGGGGGAG
 TGAGGCGGGCCGGCGCGCGCGACACCGGGCTCCGGAACCACTGCACGACGGGGCTGGACTG
 ACCTGAAAAAAATGCTCTGGATTCTTAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGG
 GAAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTGTACTATTTTTTACAGGCTGGTGGAT
 TATCATAGATGCAGCTGTTATTTATCCCACCATGAAAGATTTCAACCACTCATACCATGCCT
 GTGGTGTATAGCAACCATAGCCTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGA
 GGTGATAGTTACAGTGAAGGTTGTCTGGGTCAAACAGGTGCTCGCATTTGGCTTTTTCGTTGG
 TTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGGATTCTTTTGGAGGTTATGTTG
 CTAAAGAAAAAGACATAGTATACCCCTGGAATTGCTGTATTTTTCCAGAATGCCTTCATCTTT
 TTTGGAGGGCTGGTTTTTAAGTTTGGCCGCACTGAAGACTTATGGCAGTGAACACATCTGAT
 TTCCACAGCACAACAGCCCTGCATGGGTTGTTTGTGTTTTTACTGCTCACTCCCAACCTT
 TTGTAATGCCATTTTCTAACTTATTCTGAGTGTAGTCTCAGCTTAAAGTTGTGTAATACT
 AAAATCAGGAGAACCTTAAACAACAACCAAAAATCTATTGTGGTATGCACCTTGATTAACCT
 ATAAAAATGTTAGAGGAACTTTCACATGAATAATTTTTGTCAAATTTTATCATGGTATAATT
 TGTAAAAATAAAAAGAAATTACAAAAGAAATTATGGATTGTCAATGTAAGTATTTGTCATA
 TCTGAGGTCCAAAACCACAATGAAAGTGCTCTGAAGATTTAATGTGTTTATTCAAATGTGGT
 CTCTTCTGTGTCAAATGTTAAATGAAATATAAACATTTTTAGTTTTTAAATATTCCGTGG
 TCAAAATCTTCCTCACTATAATTGGTATTTACTTTTACCAAAAATCTGTGAACATGTAAT
 GTAACCTGGCTTTTGAGGGTCTCCCAAGGGGTGAGTGGACGTGTTGGAAGAGAGAAGCACCAT
 GGTCCAGCCACCAGGCTCCCTGTGTCCTTCCATGGGAAGGTCTCCGCTGTGCCTCTCATT
 CCAAGGCGAGGAAGATGTGACTCAGCCATGACACGTGGTCTCGGTGGGATGCACAGTCACTC
 CACATCCACCACTG

57/330

FIGURE 57

MSGFLEGLRCSECIDWGEKRNTIASIAAGVLFFTGWIIIDA AVIYPTMKDFNHSYHACGVI
ATIAFLMINAVSNGQVRGDSYSEGCLGQTGARIWLFVGFMLAFGSLIASMWILFGGYVAKEK
DIVYPGIAVFFQNAFIFFGGLVFKFGRTEDLWQ

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FIGURE 58

TTCTTGGCTAAAATCGGGGGAGTGAGGCGGGCCGCGCGCGACACCGGGCTCCGGAACC
ACTGCACGACGGGGCTGGACTGACCTGAAAAAAATGTCTGGATTCTAGAGGGCTTGAGATG
CTCAGAATGCATTGACTGGGGGGAAAAGCGCAATACTATTGCTTCCATTGTGCTGGTGTAC
TATTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGTTATTTATCCCACCATGAAAGAT
TTCAACCACTCATACCATGCCTGTGGTGTTATAGCAACCATAGCCTTCCTAATGATTAATGC
AGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTGCTCTGGGTCAACAGGTG
CTCGCATTTGGCTTTTCGTTGGTTTCATGTTGGCCTTGGATCTCTGATTGCATCTATGTGG
ATTCTTTTGGAGGTTATGTTGCTAAAGAAAAAGACATAGTATACCCTGGAATTGCTGTATT
TTTCAGAATGCCTTCATCTTTTTTGGAGGGCTGGTTTTTAAGTTTGGC

FIGURE 59

TGGACGGACCTGAAAAAATGTTTGGATTTNTAGAGGGNTTGAGATGTTTCAGAATGCATGAC
TGGGGGAAAAGCGCAAATACTATTGCTTCCATTGCTGCTGGTGTANTATTTTTACAGGCTG
GTGGATTATCATAGATGCAGNTGTTATTTATCCACCATGAAAGATTTCAACCANTCATACC
ATGCCTGTGGTGTTATAGCAACCATAGCCTTCNTAATGATTAATGCAGTATCGAATGGACAA
GTCCGAGGTGATAGTTACAGTGAAGGTGTTTGGGTCAAACAGGTGCTCGCATTGGCTTTT
CGTTGGTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGGATTCTTTTTGGAGGTT
ATGTTGCTAAAGAAAAAGACATAGTATACCCTGGAATTGNTGTATTTTTCCAGAATGCCTTC
ATCTTTTTTGGAGGGCTGGTTTTTAAGTTTGGCCGCACTGAAGANTTATGGCAGTG

FIGURE 60

GGACACCGGGTTCCGGACCAATGCANGACGGGGTGGANTGACCTGAAAAAATGTTTGGATT
TTTAGAGGGCTTGAGATGNTCAGAATGCATTGACTGGGGGAAAAGCGCAATANTATTGCTTT
CCATTGCTGCTGGTGTACTATTTTTTACAGGGTGGTGGATTATCATAGATGCAGCTGTTATT
TATCCCACCATGAAAGATTTNAACCACTCATACCATGCCTGTGGTGTATAGCAACCATAGC
CTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTT
GTTTGGGTCAAACAGGTGNTCGCATTGCGCTTTTCGTTGGTTTCATGTTGGCCTTTGGATTT
CTGATTGNATTCTATGCGGATTCTTCTTGGAGGTTATGTTGCTAAAGAAAAGACATAGTAT
ACCCTGGAATTNCTNTATTTTTCCAGAATGCC

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FIGURE 61

TAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGAAAAGCGCAATANTATTGCTTCC
ATTGNTGNTGGTGTANTATTTTTTTACAGGCTGGTGGATTATNATAGATGCAGCTGTTATTT
ATCCCACCATGAAAGATTNAACCANTCATACCATGCCTGTGGTGTTATAGCAACCATAGCC
TTCTTAATGATTAATGCAGTATNGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTG
TTGGGTCAAACAGGTGNTNGCATTTGGCTTTTNGTTGGTTTCATGTTGGCCTTTGGATCTN
TGATTGCATTTATGTGGATTNTTTTTGGAGGTTATGTTGCTAAAGNAAAAGACATAGTATAC
CCTGT

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FIGURE 62

GGGAGGCTGTGNCCTTTTGTNTTGGCTAAATCGGGGAGTGAGGCGGCCGCGCGG
CGNGACACCGGTTCCGGGAACCATTCACGACGGGGTGACTGACCTGAAAAAATGTTTG
GATTNTAGAGGCCTTGAGATGCTCAGAATGCATTGACTGGGGGAAAAGCGCAATACTATT
GCTTCATTGCTGCTGGTGACTATTTTTACAGGCTGGTGATTATCATAGATGCAGCTGT
TATTTATCCCACCATGAAAGATTTCAACCACTCATACCATGCCTGTGGTGTATAGCAACCA
TAGCCTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAA
GGTTGCTCTGGTCAAACAGGTGCTCGCATTTGGCTTTTCGTTGGTTTCATGTTGCCCTTTGG
ATNTCTGATTGCATCTATGTGGATTCTTTTGGAGGTTATGTTGCTAAAGAAAAAGACATAG
TATACCCTGGAATTGCTGTATTTTCCAGAATGCCTTCATNTTTTTTGGAGGGCTG

FIGURE 63

CGACGCCGGCGTGA**ATG**TGGCTTCCGCTGGTGTCTCTGGCTGTGCTGTGCTGCGCGTCC
TCTGCAAAAGTTTAACTTGGGACTATTCTCTGGCAGCTCCCCGAATCTTTCTCCGAAGATGTC
AAACGGCCCCGAGCGCCCTGGTAACTGACAAGGAGGCCAGGAAGAAGGTTCTCAAAACAGC
TTTTTTACGCCAACCAAGTCCCGGAGAAGCTGGAATGTGGTGGTAAATTTGGCAGTGGCTTTGGGG
GCCTTGGCTGCAGTGCAGTTCTAGCTTAAAGCTGGCAAGCGACTCTGGTGTGGAAACAACAT
ACCAAGGACAGGGGGCTGTGCTCATACCTTTGAAAGAATGGCCTTGAATTTGACACAGGAAAT
CCATTACATTTGGCGGTATGCAAGAGGCGAGCATTTGGCGGTTTTATCTGGACAGATCACTG
AAGGGCAGCTGGACTGGGCTCCCTCTCCCTCTCTCTTTTGACATCATGGTACTGGAAGGGCCC
AATGGCCGAAAGGAGTACCCCATGTACAGTGGAGAGAAGCCTACATTAGGGCCCTCAAGGA
GAAGTTTCCACAGGAGGAAGCTATCATTTGACAAGTATATAAAGCTGGTTAAGTGGTATCCA
GTGGAGCCCTCATGCCATCCTGTTGAAATTCCTCCCATTTGCCGTGGTTCAGCTCCTCGAC
AGGTGTGGGCTGCTGACTCGTTTCTCTCCATTCCTTCAAGCATCCACCAGAGCCTGGCTGA
GGTCTGACAGCAGTGGGGGGCTCCTCTGAGCTCCAGGCAGTACTCAGCTACATCTTCCCCA
CTTACGGTGTCACCCCAACCAAGTGCCTTTTCCATGCAGCGCCTGCTGGTCAACCACTAC
ATGAAAGGAGGCTTTTATCCCCGAGGGGTTCCAGTGAAATTTGCCCTCCACACCATCCCTGT
GATTCAGCGGGCTGGGGGGCTGCTCCTCAAAAGGCCACTGTGCAGAGTGTGTGTGCTGGACT
CAGCTGGGAAAGCCTGTGGTGTGAGTGTGAAGAAGGGCATGAGCTGGTGAACATCTATTGC
CCCATGCTGGTCTCCAACCGAGGACTGTTCAACACCTATGAACACCTACTGCCGGGGACAGCG
CCGCTGCTGCCAGGTGTGAAGCAGCAACTGGGGACGGTGCGGCCCGGCTTAGGCATGACCT
CTGTTTTTCATCTGCTGCGAGGCCAACGAAGAACCTGCATCTGCCGTCCACCAAGTACTAT
GTTTTACTATGACACGGACATGGACAGGCGATGGAGCGCTACGCTCCATGCCACAGGGAAGA
GGCTCGGGAAACACATCCCTCTTCTCTTCTCGCTTTCCCATCAGCCAAAGATCCGACCTGGG
AGGACCGATTCCACAGCGCGCTCCACCATGATCATGCTCATAACCTGCTTACGATGAGTGGTTT
GAGGAGTGGCAGGCGGAGTGTGAAGGGAAGCGGGGAGTGAATGAGACCTTTCAAAAACCTC
CTTTGTGTGAAGCCTCATGTCTAGTGGTCTGAAACTGTCCCAACAGCTGGAGGGGAAGGTGG
AGAGTGTGACTGCAGGATCCCCACTACCAACCAAGTTCTATCTGGCTGTCTCCCGAGGTGCC
TGCTACGGGCTGACCATGACCTTGGGCCGCTGCACCTTGTGTGATGGCCTCCTTGAGGGC
CCAGAGCCCCATCCCCAACCTCTATCTGACAGGCCAGGATATCTTCACTGTGGACTGGTTCG
GGGCCCTGCAAGGTGCCCTGCTGTGACGAGCGCCATCCTGAAGCGGAACCTGTACTCAGAC
CTTAAGAATCTTGATTCTAGGATCCGGGACAGAGAAGAAAAGAAAT**TAG**TTCCATCAGGGAGG
AGTCAGAGGAATTTGCCCAATGGCTGGGGCATCTCCCTTGACTTTACCCATAATGTCTTTCTG
CATTAGTTCTCTGACGCTATAAAGCACTCTAATTTGGTCTGTGATGCCTGAAGAGAGCCCTAG
TTTTAAATCACAATTCGAATCTGGGGCAATGGAATCACTGCTTCCAGCTGGGGCAGGTGAGA
TCTTTACGCCCTTTTATAACATGCCATCCCTACTAATAGGATATTGACTTGGATAGCTTGATG
TCTCATAGCAGCGCGCTCTGCATCCCTACCCATGCCTCCTAATCACTGATCAAAAGCGA
ATATTCCATCTGTGGATAGAACCCTGGCAGTGTGTGAGCTCAACCTGGTGGGTTTCAGTTC
TGCTCTGAGGCTTCTGCTCTCATTTAGTGCTACGCTGCACAGTTCTACACTGTCAAGG
GAAAAGGGAGACTAATGAGGCTTAACTCAAAACCTGGGCGTGGTTTTGGTTGCCATTCCATA
GGTTTTGAGAGCTCTAGATCTCTTTTTGTGCTGGGTTTCAGTGGCTCTCAGGGGACAGGAAT
GCCTGTGTCTGGCCAGTGTGGTCTGAGAGCTTTGGGTTAAACAGCAGGATCCATCAGTTAGTA
GGGTGCATGTAGATGATCATATCCAATTCATATGGAAGTCCCGGGCTGTGCTTCTTATCA
TCGGGGTGGCAGCTGGTTCTCAATGTGCCAGCAGGAGCTCAGTACCTGAGCCTCAATCAAGC
CTTATCCACCAATACACAGGGAAGGTTGATGCAGGGAAGGTTGACATCAGGAGTCAAGGCA
TGGACTGGTAAGATGAATACTTTGCTGGGCTGAAGCAGGCTGCAGGGCATTCCAGCCAAAGGG
CACAGCAGGACAGTGCAGGAGGTTGTGGGTTAAGGGAGGGAAGTCAATCAGAAAAGGGA
AAGCCACGGAATGTGTGTGAAGCCAGAAATGGCAATTTGCAAGTTAATAGCACATGTGAGGG
TTAGACAGGTAGGTGAATCAAGCTCAAGGTTTGGAAAAATGACTTTTCAGTTATGTCTTTG
GTATCAGACATACGAAGGTCCTTTTGTAGTTCGTGTTAATGTAACATTAATAAATTTATTG
ATTCCATTGCTTTAAAAA

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FIGURE 64

MWLPLVLLLAVLLLAVLCKVYLGLFSGSSPNPFSEDVKRPPAPLVTDKEARKKVLKQAFSAN
 QVPEKLDVVVIGSGFGGLAAAAILAKAGKRVLVLEQHTKAGGCCHTFGKNLEFDTGIHYIG
 RMEEGSIGRFILDQITEGQLDWAPLSSFFDIMVLEGPNGRKEYPMYSGEKAYIQGLKEKFPQ
 EEAIIDKYIKLVKVVSSGAPHAILLKFLPLFPVQLLDRCGLLTRFSPFLQASTQSLAEVLQQ
 LGASSELQAVLSYIFPTYGVTPNHSAFSMHALLVNHYMKGGFYPRGGSSEIAFHTIPVIQRA
 GGAVLTKATVQSVLLDSAGKACGVSVKKGHELVNIYCPIVVSNAGLFNTYEHLLPGNARCLP
 GVKQQLGTVRPGGMTSVFICLRGTEKEDLHLPSTNYYYYYDTDMDQAMERYVSMPREAAEH
 IPLFFAFPSAKDPTWEDRFPGRSTMIMLIPTAYEWFEEWQAEKKGKRGSDYETFKNSFVEA
 SMSVVLKLFPPQLEGKVESVTAGSPLTNQFYLAAPRGACYGADHDLGRLHPCVMASLRAQSPI
 PNLYLTGQDIFTCGLVGALQGALLCSSAILKRNLSDLNLDNRIRAQKKKN

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FIGURE 66

MRVRIGLTLLLCVLLSLASASSDEEGSQDESLSKTTLTSDSVKDHTTAGRVVAGQIFLD
SESELESSIQEEEDSLKSQEGESVTEDISFLESPNPENKDYEPPKKVRKPALTAIEGTAHG
EPCHFPPFLDKKEYDECTSDGREDGRLWCATTYDYKADEKWGFCETEEEEAAKRRQMQEAEMM
YQTGMKILNGSNKKSQKREAYRYLQKAASMNHTKALERVSYALLFGDYLPQNIQAAREMF EK
LTEEGSPKGQTALGFLYASGLGVNSSQAKALVYYTFGALGGNLI AHMVLVSRL

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FIGURE 67

CTTCCAGCCCTGTGCCCCAAAGCACCTGGAGCATATAGCCTTGCAAACTTCTACTTGCCT
GCCTCCCTGCCTCTGGCCATGGCCTGCCGGTGCCTCAGCTTCCTTCTGATGGGGACCTTCCT
GTCAGTTTCCAGACAGTCCCTGGCCCAGCTGGATGCACTGCTGGTCTTCCAGGCCAAGTGG
CTCAACTCTCCTGCACGCTCAGCCCCAGCACGTCAACATCAGGGACTACGGTGTGCTCTGG
TACCAGCAGCGGGCAGGCAGTGGCCCTCGATATCTCCTCTACTACCGCTCGGAGGAGGATCA
CCACCGGCCTGCTGACATCCCCGATCGATTCTCGGCAGCCAAGGATGAGGCCCAATGCCT
GTGTCTCACCATTAGTCCCGTGCAGCCTGAAGACGACGCGGATTACTACTGCTCTGTTGGC
TACGGCTTTAGTCCCTAGGGGTGGGGTGTGAGATGGGTGCCTCCCTCTGCCTCCATTCT
GCCCCTGACCTTGGGTCCCTTTTAAACTTCTCTGAGCCTTGCTTCCCTCTGTAAAATGGG
TTAATAATATTCAACATGTCAACAAC

68/330

FIGURE 68

MACRCLSFLLMGTFLSVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQRAG
SAPRYLLYYRSEEDHHRPADIPDRFSAKDEAHNACVLTISPVPEDDADYYCSVGYGFSF

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FIGURE 69

GCCGCCCCGCCCGAGACCGGGGCCGGGGGCGCGGGGCGCGGGGATGCGGCGCCCGGGGCGG
 CGATGACCGCGGAGCGACGCGCGGGGCCCGGCCCTGACCCCCGCCGCGCGCCGCTGAGCCG
 CCGCTCGAGGTTCGGGACGAGGCCGAGATGACCGCGAGGCCCGCTGTTGCTGCTCTGCTGCGCG
 CGCTGCTGCTGGGGGCTTCCACCGCGCGCGCGCGCGCGAGGCCCAAGAGTATGCGCGGAC
 AAGGTTGGTCCACGCGGAGGTGGCCGGCTGGGCGCGACTGTGCGGGCTGCACTGAGTCCGAGTGGG
 GGGGACCCCGCGCGCTGACCATGTGGACCAAGGATGGCGGCACCATCCACAGCTGGCTGGA
 GCGCGTTCCGCTGCTGCCGAGGGGCTGAAGGTGAAGCAGGTGGAGCGGGGAGGATGCCGCG
 GTGTACGTGTGCAAGGCGCACCAAGGCTTCGCGAGCCTGAGCGTCAACTACACCTGCTGCT
 GCTGGATGACATTAGCCAGGGAAGGAGAGCCTGGGGCCCGACAGCTCTCTGGGGGCTCAAG
 AGGACCCCGCGAGCCAGGTGGGACAGACCGGCTTCACACAGCCCTCCAAGATGAGCGCG
 CGGGTGATCGACGCGCCGTGGGTAGCTCCGCTGCGGCTCAAGTGGCTGGCCAGCGGCAACC
 TCGGCCCGACATCACGTGGATGAAGGACACAGGCTTGAACGCGCCAGGCGCGCTGAGC
 CCAGGAAGAGAACTGACACTGAGCCTGAAGACCTGCGGCGGAGGACAGCGGCAATATAC
 AACTGCGCGCTGTGCAACCGCGCGGCGGCTCAACGCGACCTACAGGTGGATGTGATCCA
 GCGGACCGGTTCAAGCCGCTGCTACAGGACGACCGCGTGAACACAGCGCTGGACTTCG
 GGGGACCGCTCTCCAGTGCAGGTGGCGAGCGAGCTGAAGCCGCTGATCCAGTGGCTG
 AAGCGCTGGAGTACGCGCGCGAGGCGCGCCACAACCTCCAGTGTGGGCGGCCAGAA
 GTTCTGTGGTGTGCTCCACCGGTGACGTGTGCTGCGCGGCCGAGCGGCTCTACCTCAATAAGC
 TGCTATCACTCCGTTGCCCGCGAGGACGATGCGGGCATGTACATCTGCCCTGGCGCCAAACCC
 ATGGGCTACAGTTCCCGACGCGCTTCTCTACCGCTGCTGCCAGACCAAAACCGCCAGGGCC
 ACCGTGGGCTCTCTGCTTCCGCGACTAGCTGCTGCGCTGGCCGCTGGTCACTCGGCATCCAG
 CCGGCGCTGTCTTATCTCTGGGACCCCTGCTCTGTGGCTTTGCCAGGCGGAGGAGAACCG
 TGCACCCCGCGGCTTCCCTTCCCTGCTGGGACCGCGCGCGGGGACGGCCGAGCCGCG
 CAGCGGAGCAAGAGACCTTCCCTGCTGGCGCGCTCAGCGCTGGCCCTGGTGTGGGGCTGT
 GTGGAGAGCATGGGTCTTCCGCGAGCCCCAGCATCTACTGGGCCCGAGGCCAGTTGCTGCG
 CCTAAGTTGTACCCAAACTCTACACAGACATCCACACACACACACACACACTCTCACAC
 ACACTACAGCTGGAGGGCAAGGTCCACAGCACATCCACTATCAGTGTAGAGGACCGCT
 ATCTGCACTGGGACCGGGGGGGCGGCCAGACAGGCAGACTGGGAGGATGGAGGACGGAGCT
 GCAGACGAAGGCGAGGGACCCATGGCGAGGAGGAATGCCAGCACCCAGCCAGGCGAGTCTGTGTG
 TGAGGACATAGCCCTGGACACACACACAGACACACACTACCTGGATGCACTGTATGCA
 ACACATGCGCGCACAGCTGCTTCCCTGAAGGCACAGGTACGCACACGCACATGACAGATATG
 CCGCTTGGGACACAGATAAGCTGCCCAATGCACGCACACGCACAGAGACATGCCAGAACA
 TACAAGGACATGCTGCTGAACATACACAGCACACCCATGCGCAGATGTGCTGCTTGGACA
 CACACACACACAGGATATGCTGTCTGGACGCACACAGTGCAGATATGGTATCCGGACACA
 CACGTGCACAGATATGCTGCTGGACACACAGATAATGCTGCTTGACACACACATGCACGG
 ATATTGCTGGACACACACACACACACAGCGTGCACAGATATGCTGTCTGGACACGCACAC
 ACATGCAGATATGCTGCTGGACACACACTTCACAGACACAGTGCACAGGCGAGATATGCT
 GCTTGGACACACGAGATATGCTGTCTAGTACACACACACGACAGACATGCTGTCCGGACAC
 ACACAGCATGACACAGATATGCTGTCCGGACACACACAGCAGCAGATATGCTGCTGGAC
 ACACACACAGATAATGCTGCTCAACACTACACACAGTGCAGATATGCTGCTGGACACACACA
 TGTGCACAGATATGCTGTCTGGACATGCACACAGTGCAGATATGCTGTCCGATACACAGC
 CAGCACACATGCAGATATGCTGCTGGGACACACTTCGGGACACACATGCACACAGGT
 GCAGATATGCTGCTGGACACACACAGATAATGCTGCTTGGGACAGCATGCTGCTGGGACAC
 CACACTGCACACACAGGTGCAGATATGCTGCTGGACACACAGCAGACTGACGTGCTTTTGG
 GAGGTTGTGCGGTGAAGCCTGCAGTACGTGTCGCTGAGGCTGAGGCTGATGATGAGGACTTT
 CCTGCTCCACGCTCACTCCCCAACTCTGCCCGCTCTGTCCCGGCTCAGTCCCGGCTC
 AGTCCCGCTCTGTGCTGGGCTGGGGTTGGGGGACAGCAGCCCCAAGCTGTGAGGCGTGGAG
 CCGTCCCTAGTGCTCATCCCCAGTGCACTTCCCTTGACACAGAGAAGGGGCTTGTA
 TTTATTTTAAAGAAATGAAGATAATATTAATAATGATGGAAGGAAGACTGGGTTCGAGGAC
 TGTGGTCTCTGGGGCGGGGACCCGCTGCTTTACGCCATGCTGATGACCAACCCG
 GTCCAGGCTCAGACACACCCGCCACCCACTGTGCTGGTGGCCCCAGATCTCTGTAAATTTTA
 TGTAGTTTGAAGTGAAGCCCCGTATTTTAATTTATTTTGAACACAAA

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MTTPSPLLLLLPLLLLGAFPPAAAARGPPKMDKVVPRQVARLGRTVRLQCPVEGDPPPLTMT
WTKDGRTIHSGWSRFRVLPQGLKVKQVEREDAGVYVCKATNGFGSLSVNYTLVLDDISPGK
ESLGPDSSSGGQEDPASQQWARPRFTQPSKMRRVIIARPVGSSVRLKCVASGHPRPDITWMK
DDQALTRPEAAEPRKKKWTLSLKNLRPEDSGKYTCRVSNRAGAINATYKVDVIQRTSRKPV
TGTHPVNTTVDFGGTTSFQCKVRSDVKPVIQWLKRVEYGAEGRHNSTIDVGGQKFFVLP
TGDVWSRPDGSYLNKLLITRARQDDAGMYICLGANTMGYSFRSAFLTVPDPKPPGPPVASSSSA
TSLPWPVVIIGIPAGAVFILGTLWLCLQAQKPKCTPAPAPPLPGHRPPGTARDRSGDKDLP
S
LAALSAGPGVGLCEEHGSAPAPQHLLGPGPVAGPKLYPKLYTDIHTHTHTSHTHSHVEGK
V
HQHIHYQC

FIGURE 71

CCGAGCTGAGGAGCCCTGCTCAAGACAGGTCCTGGATCTGAGAAACTTCCACGGGGACCGCATTTCAGAGTC
 AGTGACTCTGTGAAGACCCACATCTACCTCTTGCCACGTTCCACGGGCTGGGGGAAAGATGTTGGGGGACCA
 AGGCTCGGGTGTTCTCCTCTGGTCTGGAAGTCACATCTGTGTGGGGAGACAGACGATGCTCACCGATCA
 TGAAGAAGATCTCAGGCTGGGAAGAAGAACCCAGCATCTTTGCCAAGCCTCCGACACCCCTGGAGAGCCCTGG
 TGAATGGACACATCTGTTCAACATCGACTACCCAGGGCGGAAGGGCAGATATGAGCGGCTGGACGACATTCGCT
 TCTACTATGGGACCGGTGTATGCTCCGCTCCCTCGCGCTAGAGGCTCGGACCATCTGAGTCGAGACCTTCGCGG
 AGCATCGCTCGGCTCGCTGCTGCTCCCTGAGGCTTTCTGCTGCTCAGAGGAGCAGCGCTTCGCGCA
 GAACTGCTCTTAATTACGCTACGCTTCTCTGCCCCACAGGATCCCTGCGCGCAGACACAGAGCGCATCTGGA
 GCCCATTGTTCTCCCTGGAGCAAGTGCTCAGCTGCCCTGTGGTCAGACTGGGGTCAGACTCGCAGCACGCAATTTGC
 TTGGCAGAGATGGTGTCCGTGTGCAAGTGAGGCCAGCGAAGGCTCAGCACTGCATGGGCGAGCATGTACAGC
 CTGTGACCTGACCTTGCCCAATGGGCGAGGTGAATGCTGACTGTGATGCTGTGACTGTGCCAGGACCTTCATGCTCT
 ATGGGCTGTCTCCCTCCCGGAGGTGCCACAGCTCAGGGCTGCTATCTACCTCTGACCGAAGACCGCGAG
 CTGTGACCCGACACAGCATGATGAGATTCGGAATTCGGAATTCGCTCTGATGCGCAAAAGCATCTCGAA
 GATCACAAAGGTCAAGTTTGCCCCATTTGACTCACAATGCCAAGACTAGCTGAAGCGAGCCACCATCAAGG
 CAGAGTTTGTGAGGGCAGAGATCCATACATGGTGATGAACCTGAGACAAAAGCAGGAGCTGGGCGAGGC
 GTGTCTCTGTGCTGTGAAGGCCAGGGAAGCCAGGCCAGCAAGATATTTTGGTATCTAATGACACATTTGCT
 GGATCTCTCCCTCTACAGCATGAGACGAGCTGGTCTGAGGAACCTGACGACGACACAGGCTGGGAGGATCT
 TTTCCAGGCCAGATGATGATGAGGCTGTGAAGCTGCCCCAGCTGCTGCTCTGATGCGCAAAAGCATCTCGAA
 ACTCCTTGCAACCAAGTTCTCGAGACTATCTTATCCGGCTGCCCATGATTGCTTTTCAAGTGGCCACCACTC
 CTTCTACTATGACGTGGGACCTGCCCTGTTAAGACTGTGCGAGGCGAGCAGGATATATGGGATCAGGTGCCGTG
 ATGCTCTGCGAGAACTGCTGTGGCATCTCAAGACAGAGGAAAGGAGATCCAGTGCAGTGGCTACACGCTACCC
 ACCAAGTGTGGCCAGAGGAGTGAGCTGCCAGCGGTGTCAGGAACCTCGAGGACTGCTGCGGGGCGCTGTCACTGG
 TGCTGACATGGGGGACCCCTTCCTTTGGCCATGTCATGCGGAACGAGCTGTGAACGATCTGCTGCTTACA
 AGGCGACTTCACCTTCATGTCCTCCCGAGGACCTGAGAGGCTGCTGCTCACAATTTGTGACAGGCTGCAAG
 TTTGTCAACACCACAAAGTGCTACCTTTCAACAAGAAGGGAGTGCCTGTGTTCCATGAATCAGATGCTCTGTG
 TCGGAAGAGCCATCACTTTGGAAGCCATGGAGACCAACATCATCCCTCGGGGGAAGTGGTGTGTGAAGACC
 CTTGGCTGACATGGAGATTCCATCCAGGAGTTTTCACAGGCGAAGTGGGAGCCCTACATATGAAAAGTGAAG
 CGCATGTGCACTTCTGTGATCCCGGATATTTCCACAGCCAGCTGCCAGATGACCTGAACATCTCAAT
 TGAAGAGGACAGCACTTTCCCTTTGGGACCTGATGCAATTTCTCTGTGATCTCAGAGATGAGTCACTCAG
 AGCCACTTAATGCTGGAACAGTGAAGGTCCACCTTGACTCGACCAGGTCAGCATGCGCAGAGCATATCCACA
 GTGAAACTCTGGTCATCAATCCAGACACAGGCTGTGGGAGGAGGAAGTGATTCAAAATTTGAAATCAAG
 GAGGAACAAAAGAGAAGACAGAACCTTCTGGTGGGCAACCTGGAGATTCGTGAGAGAGGCTCTTTAACTCGG
 ATGTTCTGAAAGCAGGCGGTGCTTTGTTAAGGTGAGGGGCTACCGGAGTGAGAGGTTCTTGCTGATGAGCAG
 ATCCGCGGCTGTGATCTCCCTGATTACCTGGAGCTTGAAGCTGCTCTTGCTGCAACCTGAGGCGCTGGG
 CCGCTTTGAGATGTCATCAGAGGCCAGAGCGCTGTGCTGCTGATGATGACCATGATGACCATCCCTGATG
 CCTACTCTGCTATTTGCTTGGCAGCCCTGGCTGGGAGGAATCGAAGCAGTGGAGTGTCTCTCTAAATTCAC
 CCAATTCGAATTTGGCTGCCCTCAGCCCTATCTCAACAAGCTCAACTCCGTGGGAGGACCATGAGGATCCAG
 GGTAAAAAGACAGCTTCCAGATTAGCATGGCCAGGCCAAGGCCAAGCTCAGCTGAGGAGAGCAATGGGCGCA
 TCTATGCTTTGAGAACCTCGGCGATGTGAAGAGCCACACCAGTCGAGCCACTTCGGCTCTACAGATT
 GAGGGGATCGATATGATACACACAGCTCCCTTCACAGAGATGACCTATGAGCTGGATGAGAGATATCT
 GGCATGGTGGCCCAAGCCGATGGGATTCAGGGCTCTGATATCAAGGTGAAGATTGTGGGGCCATGGAAGTGA
 ATGTGCGATCCCGACCAATGCGGGGACCTCCTCGCGGACAGTGGGGAAGCTGTATGGAATCCGAGATGTGAGG
 AGCACTCGGGACAGGACAGCCCAATGCTCAGCTGCCCTGTCTGGATTTCAAGTCAGTGGGATGCTCTATGA
 TCAGGACGTGTGACCGCCACTGGTGAAGTCTCATCCCGAGGCGAGTCCGCTCAGGCAATGTGAACCCCA
 TCTGTCATGATGCTGCTCAACACTTGGCACTGTGATGATCAACAGCAACCTGATGAGCTGAGTCTGCGCA
 CCGCTGGAGCCACTGGGCCACAACATATGCACTCACTGACTGACAGGAGCCCTCGCAGCGCCAAAGAGAT
 CGCGCTCGCGCGGTGTGTTTGAATGACATCCGATGGCTCTCAGAAATCATGAAGAGCAATGTGGGATGATGCC
 TCACCTTCAACTCTGTGATGAGAGGCAAGTAGGCGCCAGAGTGCCCTTCAGTACTCTCAAAGACCCAGCCGAC
 TCCCTGCTGTCAGGACGTGTCAAAGGAAGTGGCTCGAGGAGGCGAGCAGGAGCAGGCGTGGGCGAGCG
 CCAAGCTGGAGTGGTGGCTCTGTGATTTCTGAGAGTGTCTCAACAGCCCTGATCAACATGAGTCTTGTGT
 ACTTCAACCTCTCTCTCTGCTGAGGCTGAGGCTGAGCTGAGCAACATGTCGCAACATGCTCTGTTTAA
 TTAAGCACTCTGTTTCTGCTGAATTTGCTTTGTTTCTTCACTGCTTACTTACTTTGTGCCATGCTACTGA
 TTGGCACTGGCCCCAACATGGCCAAATAAAGCCCTTTGTGAACCTGTTCTTTAATGAACACAGAAATTT
 GGCCACTGTGAATAACTCTGAGCTTTCAACTGTACTTTCATTTAATGCCATATATGCAATATCTTCTCTCTTT
 TCTGATGGTTTGGCCACCTCTGCAATAGTCATAATCTGATGCTGAGATCAATAACCAATATTAAGACATAT
 TTCTGGCCTGCTCGCAGGAGATAGGCAAGCTTCACTATGATCTCATGATTAATGATGATGATGATGATGAT
 AATAAAGACCAATATCTTTACTTGAATGTAAATRACTTATTTATTTCTTGTGAATTTGGAATTTCTAGTGC
 ACATTCAAGTTTAAGCTTTAAATATAGGGTGATCATAGTTCCCTTACCAGTCTGGAAGAAGCATCTCTGCTGT
 ATCCCAATTCACACAGGTTGCTAACTGTAATTTGACATTTCCCTTTCATGCTTTTGTCTTTCCTGAAGAC
 CCAGTGTAGCCGAGGCGAGATGTCAATAATGCACTACTCTGATTTTCGAAAAA

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FIGURE 72

MVGTKAWVFSFLVLETVSVLGRQTMLTQSVRRVQPGKKNPSIFAKPADTLESPEGWTTWFNI
 DYPGGKGDYERLDAIRFYGDVRCARPLRLEARTTDWTAGSTGQVVHGSPPREGFWCLNREQ
 RPGQNCNSNYTVRFLCPPGSLRRDTERIWSPWSPWKSAAACGQTGVQTRTRICLAEMVSLCS
 EASEEGQHCHMGQDCTACDLTCPMGQVNADCDACMCQDFMLHGAVSLPGGAPASGAAYLLTK
 TPKLLTQTDS DGRFRIPGLCPDGKSI LKITKVKFAPIVL TMPKTS LKAAT IKA EFVRAETPY
 MVMNPETKARRAGQSVSLCCATGKPRPDKYFWYHNDTLLDPSLYKHESKLVLRKLQQHQAG
 EYFCKAQSDAGAVKSKVAQLIVTASDETPCNFVPESYLIRLPHDCFQONATNSFYDVGRCPV
 KTCAGQQDNGIRCRDAVQNC CGISKTEEREIQCSGYTLPTKVAKESCQRCTETRSIVRGRV
 SAADNGEPMRFGHVYMGNSRVSM TGYKGTFTLHVQDTERLVLT FVDRLQKFVNTTKVLPFN
 KKGS AVFHEIKMLRRKEPITLEAMETNIIPLGEVVGEDPMAELEIPSRSFYRQNGEPYIGKV
 KASVTFLDPRNISTATAAQTDLNF INDEGDTFPLRTYGMFSVD FRDEV TSEPLNAGKVKVHL
 DSTQVKMPEHISTVKLWSLNPDTGLWEEEGDFKFENQRRNKRREDRTFLVGNLEIRERRLFNL
 DVPESRRFCVVKRAYR SERFLPSEQIQGVVISVINLEPRTGFLSNPRAWGRFDSVITGPNGA
 CVP AFCDQSPDAYSAYVLASLAGEELQAVESSPKFNPNAIGVPQPYLNKLNRYRTDHEDPR
 VKKTAFQISMAKPRPNSA EESNGPIYAFENLRACEEAPPSAAHFRFYQIEGDRYDYNTPVFN
 EDDPMSWTE DYLA WPKPMEFRACYIKVKIVGPLEVNVRSRNMGGTHRRTVGKLYGIRDVRS
 TRDRDQPNVSAACLEFKCSGMLYDQDRVDRTL VKVIPQGSRRASVNPMLHEYLVNHLPLAV
 NNDTSEYTMLAPLDPLGHNYGIYTVTDQDPRTAKEIALGRCFDGTSDGSSRIMKSNVGVALT
 FNCVERQVGRQSAFYQLQSTPAQSPAAGTVQGRVPSRRQQRASRGGRQGGVVASLRFPRVA
 QQPLIN

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FIGURE 73

CTGCAAGTTGTTAACGCCTAACACACAAGTATGTTAGGCTTCCACCAAAGTCCTCAATATACCTGAATACGCAC
 AATATCTTACTCTTCAATATTTGGTTTGGGATCTGCTTTGAGGTCCCATCTTTCATTTAAAAAAAATACAGAG
 ACTACCTTACCCGTACGCATACATACATATGTGTATATATGTAAACTAGACAAAGATCGCAGATCATAAAGC
 AAGCTCTGCTTTAGTTTCCAAGAAGATTACAAGAATTTAGAGATTGTTGTCAAGATCCCTGTCGATTCTATG
 CCCTTTGGGTTACGGTGTCTCAGTGATCGAGCCCTACCCCTTGGTTTGGGACATTATGATTTGTGTGTACAT
 CAGATTTACCGCGAAAGAGGCAAGTTTGGGATTACATGGCTCCGACGCGGAATCCACGGACATGCAAAATA
 TCTGAAGTTGAAGCTCGATCTCCGGATATTACCTGTGGAGACCCCTCTGAGACGTTCTGTGCAATGGGCAATC
 CCTACATGTGCAATATAGTGTGATGCGAGTACCCCTGAGCTGGCACACCCCCCTGAGCTGATGTTTGATTT
 GAAGGAAGACATCCCTCCACATTTTGGCAGTCTGCCACTTGAAGGAGTATCCCAAGCCTCTCCAGGTTAAAT
 CACTCTGTCTTGGAGCAAAACCATTTGAGCTAACAGACAACATAGTTATTACCTTTGAATCTGGGCGTCCAGACC
 AATGATCCTGGAGAGTCTCTCGATTATGGACGAACATGGCAGCCCTATCAGTATTATGCCACAGCTGCTTA
 GATGCTTTTCACATGGATCCTAAATCCGTGAAGGATTATACAGCATACGGTCTTAGAAATCATTTGCACAGA
 AGAGTACTCAACAGGGTATACAAACAAATAGCAAAATAATCCACTTTGAAATCAAAGACAGGTTCCGCGCTTTTG
 CTGGACCTCGCCTACGCAATATGGCTTCCCTCTACGGACAGCTGGATACAACCAAGAACTCAGAGATTTCTTT
 ACAGTACAGACCTGAGGATAAGGCTGTTAAGACCCAGCCGTTGGGAAATATTTGTAGTAGAGTACACTTGGC
 ACGTACTTTTACGCGATCTCAGACATAAAGTGGCAGGAAGGTGCAAGTGAATCTCCATGCCACTGTATGTG
 TGTATGACAACAGCAAAATGACATGCGAATGTGAGCAGAACACTACAGGTCCAGACTGTGGGAAATGCAAGAAG
 AATTATCAGGGCCGACCTTGGAGTCCAGGCTCCTATCTCCCCATCCCCAAGGCACTGCAAAATACCTGTATCCC
 CAGTATTTCCAGTATTTGGTACGAATGTCTGCGACAACAGAGCTCCTGCACTGCCAAGACGGAGGACGTGCCACA
 ACAACGTGCGCTGCTGTGCCCGGCCGATACACGGGCATCCTCTGCGAGAAGCTGCGCTGCGAGGAGGTGGC
 AGCTGCGGCTCCGACTCTGCCAGGGCGGCCCCGCCACGGCACCCACGCGCTGCTGCTGCTGACCCGCTGCT
 GGGAACCGCCAGCCCCCTGGTGTCTAGGTTGACCTCCAGGCCACACGGACGGGCGCTGTGCGTGGGGAAGCA
 GACACAACCCAAACATTTGCTACTAACATAGGAAACACACATACAGACACCCCCACTCAGACAGTGTACAAA
 CTAAGAAGGCCTAAGTGAATAGCCATATTTATCACCCGTGGACAGCACATCCGAGTCAAGACTGTTAATTTTC
 TGACTCCAGAGGAGTTGGCAGCTGTTGATATTATCACTGCAAAATCATTGCCAGCTGCAGAGCATATTGTGGA
 TTGGAAGGCTGCGACAGCCCCCAACAGGAAGACAAAAACAAACAAATCAACCGCACTAAAAACATTGGC
 TACTCTAGCGTGGTGGCCCTAGTACGACTCCGCCAGTGTGTGGACCAACAAATAGCATTTCTTGCTGTCAAG
 GTGCAATTGTGGGCATAGGAATCTGTACAGCTGCCATTGGCCGTGCTCCGCTCCCTGAATCCCTTCCAC
 CTGTGCTTTAGTGAACGTTGCTCTGTAAACCTCGTGGTTGAAAGATTTCTTTGTCTGATGTTAGTGATGCACA
 TGTGTAAACAGCCCCCTAAAGCGCAAGCCAGTCATACCCCTGTATATCTTAGCAGCACTGAGTCCAGTGCGA
 GCACACCCCACTATCAAGAGTGGCATAGGAAAAAAGAAAGTGTATCTATCCCTTTGTATTTCAATGAAGTT
 ATTTTCTTGAATCTGTAATATGTAGATTTTGTATATTGCCAATTTGTGTTACAGACAATCTGTTAAT
 GTATCTAATTCGATCAGCAAGAGCTGACATTTTATTTTGTCTCTTTCTGTTTCTGTTTCTGTTGCTGCA
 GATTTCTCTGTAAGGGCAACGAGCTGTGGCATCAAAGAAATCAGTTTACATTTTACAGGTAATAAGA
 TCCACCAAAAGCAATTTAAATGTTTCTGTTGCTTTAACTGGAAGATTAAAGAAATAAAACCTCCGCA
 TAAACGATTGAGCAATTTGATTTGCAATTTCTTAGATGAAAGGAACGCCAACAGCATTTTCACTACT
 TTAATGATTTCTGTGTGAGTGTGATCATTGAGTGAACGATTTAGTCCAGGAAGATGGATGTGATGTTCACT
 AGCTTGACACTCTCTGCAAAATATGAGACTATTTCCACTTTGGGAAAAATACACAGCAAAAAA
 AAAAAA

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FIGURE 74

MYLSRSLSIHALWVTVSSVMQPYPLVWGHYDLCKTQIYTEEGKVWDYMACQPESTDMTKYLK
VKLDPPDITCGDPPETFCAMGNPYMCNNECDASTPELAHPPELMFDFEGRHPSTFWQSATWK
EYPKPLQVNITLSWSKTIELTDNIVITFESGRPDQMLEKSLDYGRWQPYQYYATDCLDAF
HMDPKSVKDLSQHTVLEIICTEEYSTGYTTNSKIIHFEIKDRFALFAGPRLRNMASLYGQLD
TTKKLRDFFTVDLRIRLLRPAVGEIFVDELHLARYFYAISDIKVRGRCKCNLHATVCVYDN
SKLTCECEHNTTGPD CGKCKKNYQGRFWSPG SYLP I PKGTANTCIPSISSIGTNVCDNELH
CQNGGTCHNNVRCLCPAAYTGILCEKLRCEEAGSCGSDSGQGAPPHGTPALLLLTTLLGTAS
PLVF

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FIGURE 75

CCCACGCGTCCGGGTGACCTGGGCCGAGCCCTCCCGGTCGGCTAAGATTGCTGAGGAGCGG
 CGGGTAGCTGGCAGGCGCCGACTTCCGAAGGCCGCCGTCCGGGCGAGGTGTCCTCATGACTT
 CTCTTGTGGACCATGTCCTGATCTTTTTTGCCTGCGTGGTACGGGTAAGGGATGGACTGCC
 CCTCTCAGCCTCTACTGATTTTTTACCACACCCAAGATTTTTTGGAAATGGAGGAGACGGCTCA
 AGAGTTTAGCCTTGGCACTGGCCCAGTATCCAGGTGAGGTTCTGCAGAAGGTTGTGACTTT
 AGTATACATTTTTTCTTCTTTCGGGGACGTGGCCTGCATGGCTATCTGCTCCTGCCAGTGTCC
 AGCAGCCATGGCCTTCTGCTTCTGGAGACCCTGTGGTGGGAATTCACAGCTTCTATGACA
 CTACCTGCATTGGCCTAGCCTCCAGGCCATACGCTTTTCTTGAGTTTGACAGCATCATTGAG
 AAAGTGAAGTGGCATTTTAACTATGTAAGTTCCCTCAGATGGAGTGCAGCTTGGAAAAAAT
 TCAGGAGGAGCTCAAGTTGCAGCCTCCAGCGGTTCTCACTCTGGAGGACACAGATGTGGCAA
 ATGGGGTGATGAATGGTCACACACCGATGCACCTTGGAGCCTGCTCCTAATTTCCGAATGGAA
 CCAGTGACAGCCCTGGGTATCCTCTCCCTCATTTCAACATCATGTGTGCTGCCCTGAATCT
 CATTTCGAGGAGTTACCTTTCGAGAACATTCTTTACAGGATCCAAGGAGCTGGTTCTGCTGGT
 TGGACCAAACCTCGTGAAGCCAGCCACCCCTGACCCAATGAGGAGAGCTCTGATTCTCCCAT
 CCGGGAGCAGTGATGTCAAACCTCTGCTGCTGGGAAATCTCATCAGCAGGAGGCCTGTGGA
 AAAGGGCATGTCAGTGAAATCTGGGAATGGCTGGATTTCGAAACATCTGCCCATGTGATTG
 ATGGCAGAGCTGTTGCCCAAGCGCCTTTATTTAGGGTAAAATTAACAAATCCATTCTAT
 TCCTCTGACCCATGCTTAGTACATATGACCTTTAACCCTTACATTTATATGATTCGCGGTT
 GCTTCAGAAGTGTTATTTTCATGAATCATTATATGATTGATCCCCAGGATTCTATTTTGT
 TTAATGGGCTTTTCTACTAAAAGCATAAAATACTGAGGCTGATTTAGTCAGGGCAAAACCAT
 TTACTTTACATATTCGTTTTCAATACTTGCTGTTTCATGTTACACAAGCTTCTTACGGTTTTT
 TTGTAACAATAAATATTTTGAGTAAATAATGGGTACATTTTAACAAACTCAGTAGTACAACC
 TAAACTTGATAAAAGTGTGTAAAAATGTATAGCCATTATATCCTATGTATAAATTAATG
 AGGTGGCTTCAGAAATGGCAGAATAAATCTAAAGTGTTTATTAACAAAAAAGAAAAAAG
 AAAAG

FIGURE 76

MSVIFFACVVRVRDGLPLSASTDFYHTQDFLEWRRRLKSLALRLAQYPGRGSAEGCDFS IHF
SSFQDVACMAICSCQCPAAMAFCFLETLWWEFTASYDTTCIGLASRPYAFLEFDSIIQKVW
HFNYVSSSQMECSLEKIQEELKLQPPAVLTLEDTDVANGVMNGHTPMHLEPAPNFRMEPVTA
LGILSLILNIMCAALNLIRGVHLAEHSLQDPRSWFCWLDQTS

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FIGURE 77

TGCTTCCTGGAGACCCCTGTGGTGGGAATTCACAGCTTCNTATGACACTACCTGCATTGGCNT
AGCCTCCAGGCCATACGCTTTTCTTGAGTTTGACAGCATCATTCAGAAAGTGAAGTGGCATT
TTAACTATGTAAGTTCCNTNCAGATGGAGTGCAGCTTGGAAAAAATTCAGGAGGAGCTCAAG
TTGCAGCCTCCAGCGGTTCTCANTATGGAGGACACAGATGTGGCAAATGGGGT

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FIGURE 78

CTCAGCGGCGCTTCTCGTAGCGAGCCTAGTGGCGGGTGTTCGATTGAAACGTGAGCGCGA
 CCCGACCTTAAAGAGTGGGGAGCAAAGGGAGGACAGAGCCCTTAAACAGAGGCGGGTGGTG
 CCTGCCCCCTTAAAGGCGGGGCGTCCGGACGACTGTATCTGAGCCCCAGACTGCCCCGAGTT
 TCTGTGCGAGGCTGCGAGGAAAGGCCCTAGGCTGGGTCTGGGTGCTTGGCGGCGGGCTT
 CCTCCCCGCTCGTCTCCCCGGGCCAGAGGCACCTCGGCTTCAGTCACTGCTGAGCAGAGTA
AGGAAGCACTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCACGAGAGGATCCGC
 GAGTGTATTATATCAACACTTCTGTTTGCAACACTGTACATCCTCTGCCACATCTTCTGAC
 CCGCTTCAAGAAGCCTGCTGAGTTCACCACAGTGGATGATGAAGATGCCACCGTCAACAAGA
 TTGCGCTCGAGCTGTGCACCTTTACCCTGGCAATTGCCCTGGGTGCTGCTGCTGCTGCTGCCC
 TTCTCCATCATCAGCAATGAGGTGCTGCTCTCCCTGCCTCGGAACACTACATCCAGTGGCT
 CAACGGCTCCCTCATCCATGGCCTCTGGAACCTTGTTTTCTCTTCCCAACCTGTCCCTCA
 TCTTCTCATGCCCCCTTGTCATATTTCTTCACTGAGTCTGAGGGCTTTGCTGGCTCCAGAAAG
 GGTGTCCTGGGCGGGTCTATGAGACAGTGGTGATGTTGATGCTCCTCACTGCTGGTGCT
 AGGTATGGTGTGGGTGGCATCAGCCATTGTGGACAAGAACAAGGCCAACAGAGAGTCACTCT
 ATGACTTTTTGGGAGTACTATCTCCCTACCTCTACTCATGCATCTCCTTCTTGGGGTTCTG
 CTGCTCCTGGTGTGTACTCCACTGGGTCTCGCCCGCATGTTCTCCGTCACTGGGAAGCTGCT
 AGTCAAGCCCCGGCTGCTGGAAGACCTGGAGGAGCAGCTGTACTGCTACGCCTTTGAGGAGG
 CAGCCCTGACCCGAGGATCTGTAATCCTACTTCTGCTGGCTGCCTTTAGACATGGAGCTG
 CTACACAGACAGGTCTGGCTCTGCGAGACACAGAGGGTCTGCTGGAGAAGAGGGCGAAGGC
 TTACGCTTGGCAACGGAACCTGGGCTACCCCTGGCTATGCTGTGCTTGTGCTGTGCTGACGG
 GCCTGTCTGTGCTCATTGTGGCCATCCACATCCTGGAGCTGCTCATCGATGAGGCTGCCATG
 CCCCAGGCATGCAAGGTACCTCCTTAGGCCAGGTCTCCTTCTCCAAGCTGGGCTCCTTTGG
 TGCCGTCACTCAGGTTGTACTCATCTTTTACCTAATGGTGCCTCAGTTGTGGGCTTCTATA
 GCTCTCCACTCTTCCGGAGCCTGCGGCCAGATGGCACGACACTGCCATGACGCAGATAATT
 GGGAACTGTGTCTGTCTCCTGGTCCTAAGCTCAGCACTTCTGTCTTCTCTCGAACCTGGG
 GCTCACTCGCTTTGACCTGCTGGGTGACTTTGGACGCTTCAACTGGCTGGGCAATTTCTACA
 TTGTGTTCTCTACAACGCAGCCTTTGCAAGGCTCACCACACTCTGTCTGGTGAAGACCTTC
 ACTGCAGCTGTGCGGCAGAGCTGATCCGGGCCCTTTGGGCTGGACAGACTGCCGCTGCCGCT
 CTCCGGTTTCCCCAGGCATCTAGGAAGACCCAGCACCAGTGAACCTCAGCTGGGGTGGGA
 AGGAAAAAAGTGGACACTGCCATCTGCTGCCTAGGCCCTGGAGGGAAGCCCAAGCTACTTGG
 ACCTCAGGACCTGGAATCTGAGAGGGTGGGTGGCAGAGGGGAGCAGAGCCATCTGCATATT
 GCATAATCTGAGCCAGAGTTTGGGACCAGGACCTCCTGCTTTTCCATACTTAACCTGTGGCCT
 CAGCATGGGGTAGGGCTGGGTGACTGGGTCTAGCCCTGATCCCAAATCTGTTTACACATCA
 ATCTGCCCTCACTGCTGTTCTGGGCCATCCCCATAGCCATGTTTACATGATTGATGTGCAAT
 AGGGTGGGGTAGGGGAGGGAAGGACTGGGCCAGGGCAGGCTCGGGAGATAGATTGTCTCC
 CTGCTCTGCCCCAGCAGAGCCTAAGCACTGTGCTATCTCGGAGGGGCTTTGGACCACTTG
 AAAGACCAAGGGGATAGGGAGGAGGAGGCTTCAGCCATCAGCAATAAAGTTGATCCAGGGA
 AAAAAA

MEAPDYEVLSVREQLFHERIRECIISTLLFATLYILCHI FLTRFKKPAEFTTVDDEDATVVK
IALELCTFTLAIALGAVLLLLPFSIISNEVLLSLPRNYIQWLNGSLIHGLWNLVFLFPNLSL
IFLMPFAYFTESEGFAGSRKGV LGRVYETVVMLMLLTLLVLGMVWVASAIVDKNKANRESL
YDFWEYYLPYLYSCISFLGVLLLLVCTPLGLARMSVTGKLLVKPRLLEDLEEQLYCSAFEE
AALTRRICNPTSCWLPDLMELHHRQVLA LQTRVLEKKRKASAWQRNLGYPLAMLCLLVLT
GLSVLIVAIHILELLIDEAAMPGRMGQTS LGQVSFSKLSFGAVIQVVLIFYLMVSSVVGFY
SSPLFRSLRPRWHD TMTQIIGNCVCLLVSSALPVFSRTLGLTRFDLLGDGFRFNWLGNFY
IVFLYNAAFAGLTTLCVKTTAAVRAELIRAFGLDRPLPVS GFQPQASRKTQH Q

GGCTGCCGAGGGAAGGCCCTTGGGTGGTCTTGGTTGCTTGGCGGCGCGGNTTCNTCCCC
GCTCGTCTCTCCCGGGCCAGAGGCACCTTCGGCTTCAGTCATGCTGAGCAGAGTATGGAAGC
ACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCATATTCCACAGAGAGGATCCGCGAGTGTA
TTATATCAACACTTGTGTTGCAACACTGTACATCTCTCGACACTTCTCTGACCCGCTTC
AAGAAGCCTGCTGAGTTACACACAGTGGATGATGAAGATGCCACCG

GACCGACCTTAAAGAGTGGGAGCAAGGGAGGACAGAGCCTTTTAAACGAGGCGGTGGTGC
CTGCCCTTTAAGGGCGGGCGCTCCGGACGACTGTATCTGAGCCCCAGACTGCCCGAGTTTC
TGTCGAGGCTGCGAGGAAAGGCCCTAGGCTGGGTCTGGTGCTTGGCGCGCGCGGCTTCTT
CCCCGTGTGNTCCCCGGGCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTATGGA
AGCACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCACGAGAGGATCCGCGAGT
GTATTATATCAACACTTCTGTTGCAACACTGTACATCNTCTGCCACATCTTCTGACCCGC
TTCAAGAAGCCTGCTGAGTTACCACAGTGGATGATGAAGATGCCACCGTCAACAAGATTGC
GCTCGAGCTGTGCACCTTTACCTGGCAATTGCCCTGGGTGCTGTCTGCTCCTGCCCTTCT
CCATCATCAGCAATGAGGTGCTGCACTCCC

FIGURE 82

GATGTGCTCCTTGGAGCTGGTGTGCAGTGTCTTGACTGTAAGATCAAGTCCAAACCTGTTTT
GGAATTGAGGAACTTCTCTTTTGATCTCAGCCCTTGGTGGTCCAGGTCTTC**ATG**CTGCTGT
GGGTGATATTACTGGTCCTGGCTCCTGTCAAGTGGACAGTTTGCAAGGACACCCAGGCCATT
ATTTTCTCCAGCCTCCATGGACCACAGTCTTCCAAGGAGAGAGAGTGACCCTCACTTGCAA
GGGATTTCGCTTCTACTCACCACAGAAAAACAAATGGTACCATCGGTACCTTGGGAAAGAAA
TACTAAGAGAAACCCAGACAATATCCTTGAGGTTCAAGGAATCTGGAGAGTACAGATGCCAG
GCCCAGGGCTCCCTCTCAGTAGCCCTGTGCACTTGGATTTTCTTCAAGATGGGATTTCC
TCATGCTGCCAGGCTAATGTTGAACTCCTGGGCTCAAGTGATCTGCTCACC**TAG**GCCTCTC
AAAGCGCTGGGATTACAGCTTCGCTGATCCTGCAAGCTCCACTTTCTGTGTTTGAAGGAGAC
TCTGTGGTTCTGAGGTGCCGGGCAAAGCGGAAGTAACACTGAATAATACTATTTACAAGAA
TGATAATGTCCTGGCATTCTTAATAAAAGAACTGACTTCCAAAAAAAAAAAAAAAAAAAAA
AAA

FIGURE 83

MLLWVILLVLAPVSGQFARTPRPIIFLQPPWTTVFQGERVTLTCKGFRFYSPQKTKWYHRYL
GKEILRETPDNILEVQESGEYRCQAQGSPLSSPVHLDFSSEMGFPHAAQANVELLGSSDLLT

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FIGURE 84

CAGAAGAGGGGGCTAGCTAGCTGTCTCTGCGGACCAGGGAGACCCCCGCGCCCCCGGTGT
 GAGGCGGCCCTCACAGGGCCGGGTGGGCTGGCGAGCCGACGCGGCGGCGGAGGAGGCTGTGAG
 GAGTGTGTGGAACAGGACCCGGGACAGAGGAACCATGGGCTCCGCAGAACCTGAGCACCTTTT
 GCCTGTGTGCTGCTATACCTCATCGGGGCGGTGATTGCCGGACGAGATTTCTATAAGATCTTG
 GGGGTGCCTCGAAGTGCTCTATAAAGGATATTAAAAAGGCTATAGGAACTAGCCCTGCA
 GCTTCATCCCGACCGGAACCTGATGATCCACAAGCCAGGAGAAATTCAGGATCTGGGTG
 CTGCTTATGAGGTTCTGTCAGATAGTGAGAAACGGAACAGTACGATACTTATGGTGAAGAA
 GGATTAAAAGATGGTCATCAGAGCTCCCATGGAGACATTTTTTCACACTTCTTTGGGGATT
 TGGTTTCATGTTTGGAGGAACCCCTCGTCAGCAAGACAGAAATATCCAAGAGGAAGTGATA
 TTATTGTAGATCTAGAAGTCACTTTGGAAGAAGTATATGCAGGAAATTTGTGGAAGTAGTT
 AGAAACAAACCTGTGGCAAGGCAGGCTCCTGGCAAACGGAAGTGCAATTGTGCGCAAGAGAT
 GCGGACCACCCAGCTGGGCCCTGGGCGCTTCCAAATGACCCAGGAGGTGGTCTGCGACGAAT
 GCCCTAATGTCAAACCTAGTGAATGAAGAACGAACGCTGGAAGTAGAAATAGAGCCTGGGGTG
 AGAGACGGCATGGAGTACCCCTTTATTTGGAGAAGGTGAGCCTCACGTGGATGGGGAGCCTGG
 AGATTACGGTTCGGAATCAAAGTTGTCGAAGCACCCTAATATTTGAAAGGAGAGGAGATGATT
 TGTACACAAATGTGACAATCTCATTAGTTGAGTCACTGGTTGGCTTTGAGATGGATATTACT
 CACTTGGATGGTCACAAGGTACATATTTCCCGGGATAAGATCACCAGGCCAGGAGCGAAGCT
 ATGGAAGAAAGGGGAAGGGCTCCCCAACTTTGACAACAACAATATCAAGGGCTCTTTGATAA
 TCACTTTTGATGTGGATTTTCCAAAAGAACAGTTAACAGAGGAAGCGAGAGAAGGTATCAAA
 CAGCTACTGAAACAAGGGTCAGTGCAGAAGGTATACAATGGACTGCAAGGATATTGAGAGTG
 AATAAAATGGACTTTGTTTAAATAAGTGAATAAGCGATATTTATTATCTGCAAGGTTTTT
 TTGTGTGTGTTTTTGTGTTTTATTTTCAATATGCAAGTTAGGCTTAATTTTTTTATCTAATGA
 TCATCATGAAATGAATAAGAGGGCTTAAGAATTTGTCCATTGTCATTGCGAAAAGAATGACC
 AGCAAAGGTTTACTAATACCTCTCCCTTTGGGGATTTAATGCTGCTGGTGTGCCGCTGAGT
 TTCAAGAATTAAAGCTGCAAGAGGACTCCAGGAGCAAAAGAACACAATATAGAGGGTTGGA
 GTTGTTAGCAATTTCAATTCAAAATGCCAACTGGAGAAGTCTGTTTTTAAATACATTTTGTGT
 TTATTTTTTA

FIGURE 85

MAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRASIKDIKKAYRKALQLHPDRNPDDPQ
AQEKFDLGAAYEVLSDSEKRKQYDTYGEGLKDGHQSSHGDI FSHFFGDFGFMFGGTPRQQ
DRNIPRGSDIIVDLEVTLLEVYAGNFVEVVRNKPVARQAPGKRKCNCRQEMRTTQLGPGRFQ
MTQEVCVDECPCNVKLVNEERTLEVEIEPGVRDGMETPFIGEGERPHVDGEPGDLRFRIKVVKH
PIFERRGDDLYTNVTISLVESLVGFEMDITHLDGHKVVHSRDKITRPGAKLWKKGEGLPNFD
NNNIKGLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQKVYNGLQGY

Important features:**Signal peptide:**

amino acids 1-22

Cell attachment sequence.

amino acids 254-257

Nt-dnaJ domain signature.

amino acids 67-87

Homologous region to Nt-dnaJ domain proteins.

amino acids 26-58

N-glycosylation site.

amino acids 5-9, 261-265

Tyrosine kinase phosphorylation site.

amino acids 253-260

N-myristoylation site.

amino acids 18-24, 31-37, 93-99, 215-221

Amidation site.

amino acids 164-168

FIGURE 86

TGGGACCAGGGAACCCCGGGCCCCCGGTGGAGNGCCTAACAGGCCGGTGGNTGCGACCGAA
GCGGCGGGCGGAGGAGGTTTTTGAGGATTTTGGAACAGGACCCGGACAGAGGAACCATGGTT
CCGCAGAACNTGAGCACNTTTTGCCGTGTTGNTGNTATACTTCATCGGGGCGGTGATTGCCGG
ACGAGATTTNTATAAGATTTTGGGGTGCCTNGAAGTGCCTTNTATAAAGGATATTA AAAAGG
CCTATAGGAACTAGCCCTGCAGNTTATCCCGACCGGAACCCCTGATGATCCACAAGCCCAG
GAGAAATTCAGGATTTGGGTGCTGCTTATGAGGTTNTGTCAGATAGTGAGAAACGGAAACA
GTACGATAATTATGGTGAAGAAGGATTA AAAGATGGTNATCAGAGCTCCCATGGAGACATTT
TTTCACACTTNTTTGGGGATTTTGGTTTCATGTTTGAGGAACCCCTNGTCAGCAAGACAGA
AATATTCCAAGAG

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THEORY

METTVIVAIGVLATIFLASFAALVLVCRQRQYCRPDLQLQRYDSKPIVDLIGAMETQSEPSL
 ELDDVVITNPHIEAILENEDWIEDASGLMSHCIAILKICHTLLEKLVAMTMGSGAKMKTSAS
 VSDIIIVAKRISPRVDVVKSMYPPLDPKLLDARTALLSVSHLVLVTRNACHLTGGLDWI
 DQSLSAEEHLEVLREAAALASEPKLGLPPEGFLQEQSAI

FIGURE 89

GCTTCATTTCTCCGACTCAGCTTCCACCTGGGCTTCCGAGGTGCTTTCGCCGTGTCC
 CCACCACTGCAGCCATGATCTCCTTAACGGACACGCAGAAAATTGGAATGGGATTAACAGGA
 TTTGGAGTGTTTTCTTCTTTGGAATGATTCTCTTTTTTGACAAAGCACTACTGGCTAT
 TGGAAATGTTTTATTGTAGCCGGCTTGGCTTTTGTAATTGGTTTAGAAAGAACATTCAGAT
 TCTTCTCCAAAAACATAAAATGAAAGCTACAGGTTTTTTTCTGGGTGGTGTATTTGTAGTC
 CTTATTGGTTGGCCTTTGATAGGCATGATCTTCGAAATTTATGGATTTTTTCTCTTGTTCAG
 GGGCTTCTTTCTGTCTGTGTGGCTTTATTAGAAGAGTGCCAGTCCTTGGATCCCTCCTAAAT
 TTACCTGGAATTAGATCATTGTAGATAAAGTTGGAGAAAGCAACAATATGGTATTAACAACA
 AGTGAATTTGAAGACTCATTAAATATTTGTGTTATTTATAAAGTCATTTGAAGAATATTCA
 GCACAAAATTAAATTACATGAAATAGCTTGTAATGTTCTTTACAGGAGTTTAAACGTATAG
 CCTACAAAGTACCAGCAGCAAATTAGCAAAGAAGCAGTGAAAACAGGCTTCTACTCAAGTGA
 ACTAAGAAGAAGTCAGCAAGCAAACCTGAGAGAGGTGAAATCCATGTTAATGATGCTTAAGAA
 ACTCTTGAAGGCTATTTGTGTTGTTTTTCCACAATGTGCGAAACTCAGCCATCCTTAGAGAA
 CTGTGGTGCCTGTTTCTTTTCTTTTTTATTTTGAAGGCTCAGGAGCATCCATAGGCATTGCT
 TTTTAGAAGTGCCACTGCAATGGCAAAAATATTTCCAGTTGCACGTGATCTCTGGAAGTGA
 TGCATGAATTCGATTGGATTGTGTCATTTTAAAGTATTAAACCAAGGAAACCCCAATTTTG
 ATGTATGGATTACTTTTTTTTGNGCNCAGGGCC

FIGURE 90

MISLTDTQKIGMGLTGFGVFFLFFGMILFFDKALLAIGNVLFVAGLAFVIGLERTFRFFFQK
HKMKATGFFLGGVFVVLIGWPLIGMIFEIYGFFLLFRGFFPVPVVGFIIRRVPLGSLNLPGI
RSFVDKVGESNNMV

Important features:

Transmembrane domains:

amino acids 12-30 (typeII), 33-52, 69-89 and 93-109

N-myristoylation sites.

amino acids 11-16, 51-56 and 116-121

Aminoacyl-transfer RNA synthetases class-II protein.

amino acids 49-59

GAAGACGTGGCGGCTCTCGCCTGGGCTGTTTCCCGGCTTCATTCTCCCGACTCAGCTTCCC
ACCNTGGGCTTTCCGAGGTGCTTTCGCCGTGTCCCCACCCTGCAGCCATGATCTCCTTAA
CGGACACGCAGAAAAATTGGAATGGGATTAACCGGATTGGAGTGTTTTTCTGTCTTTGGA
ATGATCTCTTTTTTGACAAAGCACTACTGGCTATTGGAAATGTTTTATTGTAGCCGGCTT
GGCTTTTGAATTGGTTTTAGAAAACAATTCAGATCTCTCTTCCAAAACATAAAATGAAG
CTACAGTTTTTTTTCTGGTGGTATTGTGATCCTTATTGGTTGGCCTTTGATAGGCATG
ATCTCGAAATTTATGGATTTTTCTCTGTTC

FIGURE 92

GGCAGAGGCTGAACCCAGCCGGCTCCATCTCAGCTTCTGGTTTCTAAGTCCATGTGCCAAA
GGCTGCCAGGAAGGAGACGCCCTCCTGAGTCCTGGATCTTTCTTCTCTGGAATCTTTGA
CTGTGGGTAGTTATTATTCTGAATAAGAGCGTCCACGCATCATGACCTCGCGGGACTGC
TGAAGTCTCAGTTCTGTGCCACCTGGTCTTCTGCTACGTCTTTATTGCCTCAGGGCTAATC
ATCAACACCATTAGCTCTTCACTCTCCTCCTCTGGCCCATTAACAAGCAGCTCTTCCGGAA
GATCAACTGCAGACTGTCTATTGCATCTCAAGCCAGCTGGTGATGCTGCTGGAGTGGTGGT
CGGGCACGGAATGCACCATCTTACGGACCCGCGCGCTACCTCAAGTATGGGAAGGAAAAT
GCCATCGTGGTTCTCAACCACAAGTTTGAAATTGACTTTCTGTGTGGCTGGAGCCTGTCCGA
ACGCTTTGGGCTGTTAGGGGGCTCCAAGGTCCTGGCCAAGAAAGAGCTGGCCTATGTCCAA
TTATCGGCTGGATGTGGTACTTCACCGAGATGGTCTTCTGTTTCGCGCAAGTGGGAGCAGGAT
CGCAAGACGGTTGCCACCAAGTTTGCAGCACCTCCGGGACTACCCCGAGAAGTATTTTTCTT
GATTCACTGTGAGGGCACACGGTTTACGGAGAAGAAGCATGAGATCAGCATGCAGGTGGCCC
GGGCCAAGGGGCTGCCTCGCCTCAAGCATCACCTGTTGCCACGAACCAAGGGCTTCGCCATC
ACCGTGAGGAGCTTGAGAAATGTAGTTTCACTGTATATGACTGTACACTCAATTTAGAAA
TAATGAAATCCAACACTGCTGGGAGTCCTAAACGGAAAGAAATACCATGCAGATTTGTATG
TTAGGAGGATCCCACTGGAAGACATCCCTGAAGACGATGACGAGTGCTCGGCCTGGCTGCAC
AAGCTCTACCAGGAGAAGGATGCCTTTCAGGAGGAGTACTACAGGACGGGCACCTTCCAGA
GACGCCCATGGTGCCCCCGCGGCCCTGGACCCCTCGTGAACCTGGCTGTTTTGGGCCTCGC
TGGTGCTCTACCCCTTCTTCCAGTTCTTGGTGCAGCATGATCAGGAGCGGGTCTTCCCTGACG
CTGGCCAGCTTCATCCTCGTCTTCTTTGTGGCCTCCGTGGGAGTTCGATGGATGATTGGTGT
GACGGAATTTGACAAGGGCTCTGCCTACGGCAACTCTGACAGCAAGCAGAACTGAATGACT
GACTCAGGGAGGTGTACCATCCGAAGGGAACCTTGGGGAACCTGGTGGCCTCTGCATATCCT
CCTTAGTGGGACACGGTGACAAAGGCTGGGTGAGCCCTGCTGGGCACGGCGGAAGTCACGA
CCTCTCCAGCCAGGAGTCTGGTCTCAAGGCCGATGGGGAGGAAGATGTTTTGTAATCTTT
TTTTCCCATGTGCTTTAGTGGGCTTTGGTTTTCTTTTGTGCGAGTGTGTGTGAGAATGGC
TGTGTGGTGAGTGTGAACITTTGTCTGTGATCATAGAAGGGTATTTTAGGCTGCAGGGGAG
GGCAGGGCTGGGGACCGAAGGGGACAAGTTCCCTTTTATCCTTTGGTGTGAGTTTTCTGT
AACCTTGGTTGCCAGAGATAAAGTGAAAAGTGCTTTAGGTGAGATGACTAAATTATGCCTC
CAAGAAAAAAATTAAGTGCTTTTCTGGGTCAAAAAAAAAA

FIGURE 93

MDLAGLLKSQFLCHLVFCYVFIASGLIINTIQLFTLLLWPINKQLFRKINCRLSYCISSQLV
MLEWWSGTECTIFTDPRAYLKYGKENAIVVLNHHKFEIDFLCGWSLSERFGLLGGSKVLAKK
ELAYVPIIGWMWYFTEMVFCSRKWEQDRKTVATSLQHLDYPEKYFFLIHCEGTRFTEKKHE
ISMQVARAKGLPRLKHHLLPRTKGFAITVRSLRNVVSAVYDCTLNFRNNENPTLLGVLNGKK
YHADLYVRIPILEDIPEDDDECSAWLHKLYQEKDAFQEEYYRTGTFPETPMVPPRRPWTLVN
WLFWASLVLYPFFQFLVSMIRSGSSLTASFILVFFVASVGVRWMIGVTEIDKGSAYGNSDS
KQKLND

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FIGURE 94

CTGAGCGGGCGGTAGCA**ATG**AGGGGGAGAGTACGTCGGCGGTGCTCTCGGGCTTTGTGCTCG
 GCGCACTCGCTTTCCAGCACCTCAACACGGACTCGGACACGGAAGGTTTTCTTCTGGGGAA
 GTAAAAGGTGAAGCCAAGAACAGCATTACTGATTCCAAATGGATGATGTTGAAGTTGTTTA
 TACAATTGACATTAGAAAATATATTCCATGCTATCAGCTTTTtagctttttataattcttcag
 GCGAAGTAAATGAGCAAGCACTGAAGAAAATATTATCAAATGTCAAAAAGAATGTGGTAGGT
 TGGTACAAAATCCCGTCGTCAATTCAGATCAGATCATGACGTTTAGAGAGAGGCTGCTTCACAA
 AAACCTGCAGGAGCATTTTTCAAACCAAGACCTTGTTTTCTGCTATTAAACCAAGTATAA
 TAACAGAAAGCTGCTCTACTCATCGACTGGAACATTCTTATATAAACCTCAAAAAGGACTT
 TTTCACAGGGTACCTTTAGTGGTTGCCAATCTGGGCATGCTCTGAACAACCTGGGTTATAAAAC
 TGTATCAGGTTCCTGTATGTCCACTGGTTTTAGCCGAGCAGTACAAACACACAGCTCTAAAT
 TTTTGAAGAAGATGGATCCTTAAAGGAGGTACATAAGATAAATGAAATGTATGCTTCATTA
 CAAGAGGAATTAAGAGGTATATGCAAAAAAGTGAAGACAGTGAACAAGCAGTAGATAAACT
 AGTAAAGGATGTAAACAGATTAAACAGAGAAATTGAGAAAAGGAGAGGAGCACAGATTCAGG
 CAGCAAGAGAGAAGAATCCAAAAAGCCCTCAGGAGAACATTTTTCTTTGTGAGGCATTA
 CGGACCTTTTTTCCAAATTCGAATTTCTTCATTATGTGTTATGCTTTAAAAAATAGACA
 TGTTTCTAAAAGTAGCTGTAACACACAACCACCATCTCGATGTAGTAGACAATCTGACCTTAA
 TGGTAGAACACACTGACATTCTGAAGCTAGTCCAGCTAGTACACCACAAATCATTAAAGCAT
 AAAGCCTTAGACTTAGATGACAGATGGCAATTCAAGAGATCTCGGTTGGTTAGATACACAAGA
 CAAACGATCTAAAGCAAATACTGGTAGTAGTAACCAAGATAAAGCATCCAAAATGAGCAGCC
 CAGAAACAGATGAAGAAATTGAAAAGATGAAGGGTTTTGGTGAATATTACGGCTCTCTACA
 TTT**TGA**TCCCTTTTAACCTTACAAGGAGATTTTTTTATTTGGCTGATGGGTAAAGCCAAACAT
 TTCTATTGTTTTTACTATGTTGAGCTACTTGCAGTAAGTTCACTTTGTTTTTACTATGTTTAC
 CTGTTTGCAAGTAATACACAGATAACTCTTAGTGCATTTACTTCAAAAGTACTTTTTCAAAC
 ATCAGATGCTTTTATTTCCAAACCTTTTTTTTACCTTTCACTAAGTTGTTGAGGGGAAGGCT
 TACACAGACACATTCTTTAGAATTGGAAGTGAAGACAGGCACAGTGGCTCACACCTGTAA
 TCCAGCACTTAGGGGAAGACAAGTCAGGAGGATTGATTGAAGCTAGAGTTAGAGACCAGCC
 TGGGCAACGTATTGAGACCATGTCTATTAATAAATAAATGGAAGCAAGAATAGCCTTAT
 TTTCAAAATATGGAAGAAATTTATATGAAAATTTATCTGAGTCATTAAATTTCTCCTTAAG
 TGATACTTTTTTGAAGTACATTATGGCTAGAGTTGCCAGATAAAATGCTGGATATCATGCA
 ATAAATTTGCAAAACATCATCTAAAATTTAAAAAAAAAAAAAAAAAAAAA

FIGURE 95

MEGESTSAVLSGFVLGALAFQHLNTDSDTEGFLLGEVKGEAKNSITDSQMDDVEVVYTIDIQ
KYIPCYQLFSFYNSSGEVNEQALKILSNVKNVVGWYKFRRHSDQIMTFRERLLHKNLQEH
FSNQDLVFLLLTPSIITESCSTHRLEHSLYKPQKGLFHRVPLVVANLGMSEQLGYKTVSGSC
MSTGFSRAVQTHSSKFFEEEDGSLKEVHKINEMYASLQEELKSICKKVEDSEQAVDKLVKDVN
RLKREIEKRGAQIQAAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMSLKNRHVSKSS
CNYNHHLDVVDNLTLMEHTDIPEASPASTPQIIKHKALDLDDRWQFKRSRLLDTDKRSKA
NTGSSNQDKASKMSSPETDEEIEKMKGFGEYSRSPTF

FIGURE 96

GGCACAGCCGCGCGCGGAGGGCAGAGTCAGCCGAGCCGAGTCCAGCCGAGCAGAGCGGACAGCGCAGGGCAGC
 CCAAGCAGCGCGCAGCGAACGCCCGCCGCGCCACACCCCTCTGCGGTCCCGCGGGCGCTGCCACCCCTTCCTCT
 CCTTCCCGCGGTCCCGCCTCGCCGCGCAGTCAGCTTGCCGGTTTCGTGCCCGCGGAAACCCCGAGGTACACCA
 GCGCCGCGCTCTGCTTCCCTGGGCGCGCGCGCCTCCAGCCCTCCCTTCCCTGGCCGCGCGCTGGCACC
 GGGGACCGTGGCTGACGCGAGGCCAGCTCTACTTTTCCCGCGCGTCTCTCCGCGTGTCTCGCCTCTTCCAC
 CAACTCCAACTCCTCTCCCTCCAGCTCCACTCGCTAGTCCCCGACTCCGCCAGCCCTCGGCCGCTCGCGGTAG
 CGCCGCTTCCGCTCGCGTCCAAAGTGGAAACGCTCCGCCCGCGCCGACAGTGGACCGTTCCGCTTGC
 CGCGCTTCTCTGCACCTGGCAGTGCTCAGCGCGCGCTGCTGGCTGCCAGCTCAAGTCGAAAGATTGCTCG
 AAGTGGCAGCTCTTACGTGTCCAAAGGCTTCAACAAGAACGATGCCCTCCAGAGATCAACGGTGATCAT
 TTGAAGATCTGTCCCAGGGTTCTACCTGCTGCTCTCAAGAGATGGAGGAGAAGTACAGCCTGCAAAAGTAAGA
 TGATTTCAAAGTGTGGTCAGCGAACAGTGAATCATTTGCAAGCTGTCTTTGCTTACGTTACAAGAAGTTTG
 ATGAATTTCTCAAAGAACTACTTGAAAATGACAGAGAAATCCCTGAATGATATGTTTGTGAAGACATATGCCAT
 TTATACATGCAAAATTTCTGAGCTATTTAAAGATCTCTTCGTAGAGTTGAAACGTTACTACGTGGTGGGAAATGT
 GAACCTGGAAGAAATGCTAAATGACTTCTGGGCTCGCCTCCTGGAGCGGATGTTCCGCTGGTGAATCCAGT
 ACCACTTTACAGATGAGTATCTGGAATGTGTGAGCAAGTATACGGAGCAGCTGAAGCCCTTCGGAGATGTCCCT
 CGCAAAATTGAAGCTCCAGGTTACTCGTGCTTTTGTAGCAGCCGTACTTTCCGTCGAAGGCTTAGCGGTTGCGGG
 AGATGTCGTGAGCAAGTCTCCGTGGTAAACCCACAGCCAGTGTACCCATGCCCTGTTGAAGATGATCTACT
 GCTCCCACTCGCGGGTCTCGTGACTGTGAAGCCATGTTACAACTACTGCTCAAACATCATGAGAGGCTGTTTG
 GCCAACCAAGGGGATCTCGATTTTGAATGGAACAATTTCTATAGATGCTATGCTGATGGTGGCAGAGAGGCTAGA
 GGGTCTTTCAACATTTGAATCGGTATGGATCCCATCGATGTGAAGATTTCTGATGCTATTATGAACATGCAGG
 ATAATAGTGTTCAGTGTCTCAGAAGGTTTCCAGGGATGTGGACCCCCCAAGCCCTCCAGCTGGACGAAT
 TCTCGTTCATCTCTGAAAGTGCTTCACTGCTCGCTTCAAGCCACATCACCCAGGAAACGCCCAACACAGC
 AGCTGGCACTAGTTTGGACCGACTGGTTACTGATGTCAAGGAGAACTGAAACAGGCCAAGAAATTTCTGGTCT
 CCCTTCGAGCAACGTTTGAACGATGAGAGGATGGCTGCAGGAAACGGCAATGAGGATGACTGTTGGAATGG
 AAAGGCAAAAGCAGGTACCTGTTTCAGTGCAGGAAATGGATAGCCAACAGGCGAACACCCAGAGGTCCA
 GGTGACACCAGCAACACAGACATCTGATCCTTCGTCAATCATGGCTTTCAGTGTATGACCAGCAAGATGA
 AGAATGCATACATGGAACGACCTGGACTTCTTGATATCAGTGATGAAAGTAGTGAGAGAGGAGTGGAGT
 GGCTGTGAGTATCAGCAGTGGCCTTCAAGTTTGAATACATGCCACTGACCATGCTGGGAGAGTGCCATGA
 GAAAGCCGACAGTGTGGTGTCCGTCTGGGACAGGCCCTACCTCCTCACTGTCTCTGATCTTGTTCCTGG
 TTATCGAGAGAGTGGAGATTAATCTCAAACCTGAGAAAAAGTGTTCTCAAAGTTAAAGGCCACGATT
 ATCAGTTTTCTACCATCTAGTGACTTTGCTTTTAAATGAATGGACAAATGTACAGTTTTCATATGTGGC
 CACTGGTTTAAAGAGTGTGACTTTGTTTCTCATTGCTTTGGGAGGAAAGGAGCTGTGCATTGAGTTGGT
 TCTGCTCCCCAAACCATCTTAAACCTGGCTAACAGTGTAGTACAGACTATAGTTAGTTGTGATTTTGTA
 TTTTACACTCTATTATTTTGTATGTTTCTTCTCAITTCGTTTGTGGGTTTCTTTTCCAACTGTGATCT
 CGCCTTGTCTTACAGCAACACAGGTCCTTCTTGGCAGCTAACATGTACGTATTTCTGAAATATTAATA
 GCTGTACAGAAGCAGGTTTATTTATCATGTTATCTTATTAAGAAAAAGGCCAAAGC

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FIGURE 97

MARFGLPALLCTLAVLSAALLAAELKSKSCSEVRRLYVSKGFNKNDAPLHEINGDHLKICPQ
GSTCCSQEMEEKYSLQSKDDFKSVVSEQCNHLQAVFASRYKKFDEFFKELLENAEKSLNDMF
VKTYGHLVMQNSSELFKDLFVELKRYVVGNNLEEMLNDFWARLLERMFRLVNSQYHFTDEY
LECVSKYTEQLKPFPGDVPRKLLQVTRAFVAARTFAQGLAVAGDVVSKVSVVNPTAQCTHAL
LKMIYCSHCRGLVTVKPCYNYCSNIMRGCLANQGDLD FEWNNFIDAMLVAERLEGPFNIES
VMDPIDVKISDAIMNMQDNSVQVSQKV FQGC GPPKPLPAGRISRISSESASF SARFRPHHPEE
RPTTAAGTSLDRLVTDVKEKLKQAKKFWSSLPSNVCNDERMAAGNGNEDDCWNGKGKSRYLE
AVTGNGLANQGNNPEVQVDTSKPDILILRQIMALRVMTSKMKNAYNGNDVDFDISDESSGE
GSGSGCEYQQCPSEFDYNATDHAGKSANEKADSAGVRPGAQAYLLTVFCILFLVMQREWR

FIGURE 98

CTCGCCCTCAAATGGGAACGCTGGCCTGGGACTAAAGCATAGACCACCAGGCTGAGTATCCT
GACCTGAGTCATCCCCAGGGATCAGGAGCCTCCAGCAGGGAACCTTCCATTATATTCTTCAA
GCAACTTACAGCTGCACCGACAGTTGCGATGAAAAGTTCTAATCTCTTCCCTCCTCCTGTTGC
TGCCACTAATGCTGATGTCCATGGTCTCTAGCAGCCTGAATCCAGGGGTCGCCAGAGGCCAC
AGGGACCGAGGCCAGGCTTCTAGGAGATGGCTCCAGGAAGGCGGCCAAGAATGTGAGTGCAA
AGATTGGTTCTGAGAGCCCCGAGAAGAAAATTCATGACAGTGTCTGGGCTGCCAAGAAGC
AGTGCCCTGTGATCATTTCAAGGGCAATGTGAAGAAAACAAGACACCAAGGCACCACAGA
AAGCCAAACAAGCATTCCAGAGCCTGCCAGCAATTTCTCAAACAATGTCAGCTAAGAAGCTT
TGCTCTGCCTTTGTAGGAGCTCTGAGCGCCCACTCTTCCAATTAACATTCTCAGCCAAGAA
GACAGTGAGCACACCTACCAGACACTCTTCTTCTCCACCTCACTCTCCCACTGTACCCACC
CCTAAATCATTCAGTGCTCTCAAAAAGCATGTTTTTCAAGATCATTTTGTGTTGTGCTCTC
TCTAGTGTCTTCTTCTCTCGTCAGTCTTAGCCTGTGCCCTCCCCTTACCAGGCTTAGGCTT
AATTACCTGAAAGATTCCAGGAACTGTAGCTTCTAGCTAGTGTCAATTTAACCTTAAATGC
AATCAGGAAAGTAGCAAAACAGAAGTCAATAAATATTTTAAATGTCAAAAAAAAAAAAAAAAAA

FIGURE 99

MKVLISLLLLLPLMLMSMVSSSLNPGVARGHRDRGQASRRWLQEGGQECECKDWFLRAPRR
KFMTVSGLPKKQCPCDHFKNVKKTRHQRHHRKPNKHSRACQQFLKQCQLRSFALPL

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T09TTT.T8TTT660

FIGURE 100

AATGGCTGTCTTAGTACTTCGCCTGACAGTTGTCTCTGGGACTGCTTGTCTTATTCCTGACCT
GCTATGCAGACGACAAACCAGACAAGCCAGACGACAAGCCAGACGACTCGGGCAAAGACCCA
AAGCCAGACTTCCCCAAATTCTAAGCCTCCTGGGCACAGAGATCATTGAGAATGCAGTCGA
GTTTCATCCTCCGCTCCATGTCCAGGAGCACAGGATTTATGGAATTTGATGATAATGAAGGAA
AACATTTCATCAAAGTGAACATCCTCAGGACACACCCATGTGGCTCCTGGACAATCCAAGAGCA
GCCAAATCCTGCTTTTCCAGTTTGGCTCCACAAGTCCTCCAGGACAGAGCCCTCAAAGCAAC
TCCCAACGAGTTCTCAGGATTCAGGCTCTGGCTTCAACCAACAGAACTCATTTTGAACACC
CTGACTGCATTTTGTCTTTAGAAAGTTAGAATAAATATGGCGCTTTGGGATCACATAGTTG
ATGGAGAGGAAA

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101/330

FIGURE 101

MAVLVLRLTVVLGLLVLF LTCYADDKPKDPDDSGKDKPDPFKFLSLLGTEIIENAVE
FILRSMRSTGFMEFDDNEGKHSSK

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FIGURE 102

GGATGCCAGCGCCTGCAGAGGCTGAGCAGGGA AAAAGCCAGTGCCCCAGCGGAAGCACAGCT
 CAGAGCTGGTCTGCCATGGACATCCTGGTCCCACTCCTGCAGCTGCTGGTGCTGCTTCTTAC
 CCTGCCCCTGACCTCATGGCTCTGCTGGGCTGCTGGCAGCCCCGTGTGCAAAAGCTACTTCC
 CCTACCTGATGGCCGTGCTGACTCCCAAGAGCAACCGCAAGATGGAGAGCAAGAAACGGGAG
 CTCTTCAGCCAGATAAAGGGGCTTACAGGAGCCTCCGGGAAAGTGGCCCTACTGGAGCTGGG
 CTGCGGAACCGAGGCCAACTTTCAGTTCTACCCACCGGGCTGCAGGGTCACCTGCCTAGACC
 CAAATCCCCACTTTGAGAAGTTCCTGACAAAGAGCATGGCTGAGAACAGGCACCTCCAATAT
 GAGCGGTTTGTGGTGGCTCCTGGAGAGGACATGAGACAGCTGGCTGATGGCTCCATGGATGT
 GGTGGTCTGCACTCTGGTGCTGTGCTCTGTGCAGAGCCCAAGGAAGGTCTGCAGGAGGTCC
 GGAGAGTACTGAGACCGGGAGGTGTGCTCTTTTTCTGGGAGCATGTGGCAGAACCATATGGA
 AGCTGGGCCCTTCATGTGGCAGCAAGTTTTCGAGCCCACTGGAAACACATTGGGGATGGCTG
 CTGCCTCACCAGAGAGACCTGGAAGGATCTTGAGAACGCCAGTTCTCCGAAATCCAAATGG
 AACGACAGCCCCCTCCCTGAAGTGGCTACCTGTTGGGCCCCACATCATGGGAAAGGCTGTC
 AAACAATCTTTCCCAAGCTCCAAGGCACTCATTTGCTCCTTCCCCAGCCTCCAATTAGAACA
 AGCCACCCACCAGCCTATCTATCTTCCACTGAGAGGGACCTTAGCAGAATGAGAGAAGACATT
 CATGTACCACCTACTAGTCCCTCTCTCCCCAACCTCTGCCAGGGCAATCTCTAACTTCAATC
 CCGCCTTCGACAGTGAAAAAGCTCTACTTCTACGCTGACCCAGGGAGGAAACACTAGGACCC
 TGTGTATCCTCAACTGCAAGTTTCTGGACTAGTCTCCCAACGTTTGCCTCCCAATGTTGTC
 CCTTTCCTTCGTTCCCATGGTAAGCTCCTCTCGCTTTCCTCCTGAGGCTACACCCATGCGT
 CTCTAGGAACCTGGTCACAAAAGTCATGGTGCCTGCATCCCTGCCAAGCCCCCTGACCTCT
 CTCCCCACTACCACCTTCTTCTGAGCTGGGGGACCAGGGAGAATCAGAGATGCTGGGGAT
 GCCAGAGCAAGACTCAAAGAGGCAGAGGTTTGTCTCAAAATATTTTAAATAAATAGACGA
 AACCACG

MDILVPLLQLLVLLLTLPPLHLMA LLGCWQPLCKSYFPYLMAVLTPKSNRKMESKKRELFSQI
KGLTGASGKVALLELGC GTGANFQFYPGGRV TCLDPNPHFEKFLT KSM AENRH LQYERFV
APGEDMRQLADGSDMVVVCTLTLC SVQSPRKVLQEVRRVLRPGGVLF FWEHVAEPYGSWAF
WQVFEPTFKHIGDCCLTR ETWKDLENAQFSEIQMERQFPLKWLVPVGHIMGKAVKQSF
SSKALIKSPHSLQEQATHPTIYPLRGT

FIGURE 104

GTGGGATTTATTTTGAGTGCAAGATCGTTTTCTCAGTGGTGGTGGAAAGTTGCCTCATCGCAGG
 CAGATGTTGGGGCTTTGTCCGAACAGCTCCCCCTCTGCCAGCTTCTGTAGATAAGGGTTAAAA
 ACTAATATTTATATGACAGAAGAAAAAGATGTCATTCCGTAAAGTAAACATCATCATCTTGG
 TCCTGGCTGTTGCTCTCTTCTTACTGGTTTTGCACCATAACTTCTCTCAGCTTGAGCAGTTTG
 TTAAGGAATGAGGTTACAGATTGAGGAATTTGAGGGCCTCAACCTATAGACTTTGTCCCAAA
 TGCTCTCCGACATGCAGTAGATGGGAGACAAGAGGAGATTCTGTGGTCATCGCTGCATCTG
 AAGACAGGCTTGGGGGGGCCATTGCAGCTATAAACAGCATTTCAGCACAACTCGCTCCAAT
 GTGATTTTCTACATTGTTACTCTCAACAATACAGCAGACCATCTCCGGTCTGGCTCAACAG
 TGATTCCTGAAAAGCATCAGATACAAAATTGTCAATTTTGACCTAACTTTTGGAAGGAA
 AAGTAAAGGAGGATCCTGACCAGGGGAATCCATGAAACCTTTAACCTTTGCAAGGTTCTAC
 TTGCCAATTTCTGGTTCAGCGCAAAGAAGGCCATATACATGGATGATGATGTAATTGTGCA
 AGGTGATATTCTTGCCCTTTACAATACAGCACTGAAGCCAGGACATGCAGCTGCATTTTCAG
 AAGATTGTGATTCAGCCTCTACTAAAAGTTGTATCCGTGGAGCAGGAAACCAGTACAATTAC
 ATTGGCTATCTTGACTATAAAAAGGAAAGAATTTCGTAAGCTTTCCATGAAAGCCAGCACTTG
 CTCATTTAATCCTGGAGTTTTTGTGCAACCTGACGGAATGGAACGCAGACAATATAACTA
 ACCAACTGGA AAAATGGATGAAACTCAATGTAGAAGAGGGACTGTATAGCAGAACCCTGGCT
 GGTAGCATCACAAACCTCCTCTGCTTATCGTATTTTATCAACAGCACTCTACCATCGATCC
 TATGTGGAATGTCGCCACCTTTGGTTCCAGTGCTGGAACGATATTCACTCAGTTTGTAA
 AGGCTGCCAAGTTACTCCATTGGAATGGACATTTGAAGCCATGGGGAAGGACTGCTTCATAT
 ACTGATGTTTGGGAAAAATGGTATATTCCAGACCCAACAGGCAAATTC AACCTAATCCGAAG
 ATATACCAGATCTCAAACATAAAGTGAACAGAAATTTGAACTGTAAGCAAGCATTCTCAG
 GAAGTCCTGGAAGATAGCATGCATGGGAAGTAACAGTTGCTAGGCTTCAATGCCTATCGGTA
 GCAAGCCATGGA AAAAGATGTGTGAGCTAGGTAAAGATGACAACTGCCCTGTCTGGCAGTC
 AGCTTCCAGACAGACTATAGACTATAAATATGTCTCCATCTGCCCTACCAAGTGTCTTCTT
 ACTACAATGCTGAATGACTGGAAGAAGAACTGATATGGCTAGTTACAGTACGCTGGTACAGA
 TAATTCAAACTGCTGTTGGTTTTAATTTTGTAACTGTGGCTGATCTGTAATAAACTT
 ACATTTTTTC

FIGURE 105

MSFRKVNIIILVLAVALFLLVLHNFSLSSLRNEVTDSGIVGPQPIDFVPNALRHAVDGR
QEEIPVVIAASEDRLGGAIAAINS IQHNTRS NVIFYIVTLNNTADHLRSWLNSDSLKSIRYK
IVNFDPKLLEGKVKEDPDQGESMKPLTFARFYLPILVPSAKKAIYMDDDVIVQG DILALYNT
ALKPGHAAAFSEDCDSASTKV VIRGAGNQNYIGYLDYKKERIRKLSMKASTCSFNPGVFVA
NLTEWKRQNITNQLEKWMKLNVEEGLYSRTL AGSITTPLLIVFYQQHSTIDPMWNVRLGS
SAGKRYSPQFVKA AKLLHWNHGLKPWGRTASYTDVWEKWYIPDPTGKFNLIRRYTEISNIK

105/330

FIGURE 106

TGGTTTTTGGCCCATAAATTCCTCAGCTTGAGCAGTTTGTTAAGGAATGAGGTTACAGATT
CAGGAATTNTAGGNCCTCAACCTNTAGANTTTGTCCCAAATGTTCTCCGACATGCAGTAGAT
GGGAGACAAGAGGAGATTCTGTGGTCATCGCTGCATNTGAAGACAGGCTTGGGGGGGCCAT
TGCAGCTATAAACAGCATTCAGCACAACTCGNTCCAATGTGATTTTCTACATTGTTACTC
TCAACAATACAGCAGACCATNTCCGGTCCTGGNTCAACAGTGATTCCCTGAAAAGCATCAGA
TACAAAATTGTCAATTTTGACCCTAAACTTTTGAAGGAAAAGTAAAGGAGGATCCTGACCA
GGGGGAATCCATGAAACCTTTAACCTTTGCAAGGTTCTACTTGCCAATTCTGGTTCACAGCG
CAAAGAAGGCCATATACATGGATGATGATGTAATTGTGCAAGGTGATATTCTTGCCCTTTAC
AATACAGCACTGAAGCCAGGACATGCAGCTGCATTTTCAGAAGATTGTGATTCAGCCTCTAC
TAAAGTTGTCATCCGTGGAGCAGGAAA

FIGURE 107

CGACGCTCTAGCGGTTACCGCTGCGGGCTGGCTGGGCGTAGTGGGGCTGCGCGGCTGCCACG
 GAGCTAGAGGGCAAGTGTGCTCGGCCAGCGTGCAGGGAACGCGGGCGGCCAGACAACGGGC
 TGGGCTCCGGGGCTGCGGCGCGGGCGCTGAGCTGGCAGGCGGGTCCGGGCGCGGGCTGCA
 TCCGCATCTCCTCCATCGCCTGCAGTAAGGGCGGCCGCGGCGAGCCTTTGAGGGGAACGACT
 TGTGCGAGCCCTAACAGGGGTGTCTCTGAGCCTGGTGGGATCCCCGAGCGTCACATCACT
 TTCCGATCACTTCAAAGTGGTTAAAACTAATATTTATATGACAGAAGAAAAAGATGTCATT
 CCGTAAAGTAAACATCATCATCTTGGTCTGGGCTGTTGCTCTCTTCTTACTGGTTTTGCAC
 CATAACTTCTCAGCTTGAGGCAGTTTGTTAAGGAATGAGGTTACAGATTGAGGAATTGTAG
 GGCCTCAACCTATAGGACTTTGTCCCAAATGCTCTCCGACATGCAGTAGATGGGAGACAAGA
 GGAGATTCTGTGGTCATCGCTGCATCTGAAGACAGGCTTGGGGGGGCCATTGCAGCTATAA
 ACAGCATTGAGCACAACACTCGCTCCAATGTGATTTTCTACATTGTTACTCTCAACAATACA
 GCAGACCATCTCCGGTCCTGGGCTCAACAGTGATTCCCTGAAAAGCATCAGATACAAAATTG
 TCAATTTTGACCCTAAACTTTTGAAGGAAAAGTAAAGGAGGATCCTGACCAGGGGGAATCC
 ATGAAACCTTTAACCTTTGCAAGGTTCTACTTGCCAATTCTGGGTTCCAGCGCAAGAAGG
 CCATATACATGGATGATGATGTAATTGTGCAAGTGATATTCTTGCCCTTTACAATACAGCA
 CTGAAGCCAGGACATGCAGCTGCATTTTCAGAAGATTGTGATTGAGCCTCTACTAAAGTTGT
 CATCCGTGGAGCAGGAACCAAGTACAATTACATTGGCTATCTTGACTATAAAAAGGAAAGAA
 TTCGTAAGCTTTCATGAAAGCCAGCACTTGCTCATTTAATCCTGGAGTTTTTGTGCAAAC
 TTGACGGAATGGAACGACAGAATATAACTAACCAACTGGAAAAATGGATGAAACTCAATGT
 AGAAGAGGGACTGTATAGCAGAACCCTGGCTGGTAGCATCACAACACCTCCTCTGCTTATCG
 TATTTTTATCAACAGCACTCTACCATCGATCCTATGTGGAATGTCCGCCACCTTGGTCCAGT
 GCTGGAAAAAGCATATTACCTCAGTTTGTAAGGCTGCCAAGTTACTCCATTGGAATGGACA
 TTTGAAGCCATGGGGAAGGACTGCTTCATATACTGATGTTTGGGGAAAAATGGTATATTCCA
 GACCAACAGGCAAAATCAACCTAATCCGAAGATATACCGAGATCTCAAACATAAAGTGAAA
 CAGAATTTGAAGTGTAAAGCAAGCATTCTCAGGAAGTCCCTGGAAGATAGCATGCGTGGGAAG
 TAACAGTTGCTAGGCTTCAATGCCTATCGGTAGCAAGCCATGAAAAAAGATGTGTGAGCTAG
 GTAAAGATGACAAACTGCCTGTCTGGCAGTCAGCTTCCAGACAGACTATAGACTATAAAT
 ATGTCTCCATCTGCCTTACCAAGTGTCTTCTTACTACAAATGCTGAATGACTGGAAGAAGAA
 CTGATATGGCTAGTTCAGCTAGCTGGTACAGATAATTCAAACCTGCTGTTGGTTTTAATTTT
 GTAACTGTGGCCTGATCTGTAAATAAACTTACATTTTTCAATAGGTAAAAAAGAAAAA
 AAAAA

FIGURE 108

CTGCAGGTAGACATCTCCACTGCCCAGGAATCACTGAGCGTGCAGACAGCACAGCCTCCTCT
GAAGGCCGGCCATACCAGAGTCCTGCCTCGGCATGGGCCTCACCATTGAGGCAGCTCCACTG
TCTGTGCTGGTCTGAGGGTGCTGCCTGTCATGGGGGCAGCCATCTCCCAGGGGGCCCTCATC
GCCATCGTCTGCAACGGTCTCGTGGGCTTCTTGCTGCTGCTGCTGCTGGGTCACTCTGCTG
GGCCTGCCATTCTCGTCTGCCGACGTTGACTCTCTCTCTGAATCCAGTCCCAACTCCAGCCC
TGGCCCTGTCTTGAGAAGGCCCCACCACCCAGAAGCCCAGCCATGAAGGCAGCTACCTGC
TGCAGCCCTGAAGGCCCTGGCCTAGCCTGGAGCCCAGGACCTAAGTCCACCTCACCTAGAG
CCTGGAATTAGGATCCCAGAGTTCAGCCAGCCTGGGGTCCAGAACTCAAGAGTCGCCTGCT
TGGAGCTGGACCCAGCGGCCAGAGTCTAGCCAGCTTGGCTCCAATAGGAGCTCAGTGGCCC
TAAGGAGATGGGCCTGGGGTGGGGCTTATGAGTTGGTGCTAGAGCCAGGGCCATCTGGACT
ATGCTCCATCCCAAGGGCCAAGGGTCAGGGGCCGGGTCCACTCTTTCCCTAGGCTGAGCACC
TCTAGGCCCTCTAGGTTGGGAAGCAAACCTGGAACCCATGGCAATAATAGGAGGGTGTCCAG
GCTGGGCCCTCCCCTGGTCTCCAGTGTCTTGCTGGATAATAAATGGAACCTATGGCTCTAA
AAAAAAAAAAAAAAAAA

109/330

FIGURE 109

MGAATISQGALIAIVCNGLVGFLLLLWVILCWACHSRLPTLTLSLNPVPTPALAPVLRPHH
PRSPAMKAATCCSPEGPWPSLEPRT

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GTTTGAATTCCTTCAACTATACCCACAGTCCAAAAGCAGACTCACTGTGTCCAGGCTACCA
GTTCTCTCCAAGCAAGTCATTTCCCTTATTTAACCGATGTGTCCCTCAAACACCTGAGTGCTA
CTCCCTATTTGCATCTGTTTTGATAAATGATGTTGACACCCCTCCACCGAATTCTAAGTGGAA
TCATGTCGGGAAGAGATACAATCCTTGGCCTGTGTATCCTCGCATTAGCCTTGTCTTTGGCC
ATGATGTTTACCTTCAGATTCATCACCACCCCTTCTGGTTCACATTTTCATTTCATTGTTAT
TTTGGGATTGTTGTTTGTCTGCGGTGTTTATGTGGCTGTATTATGACTATACCAACGACC
TCAGCATAGAATTGGACACAGAAAGGGAAAAATATGAAGTGCCTGCTGGGGTTTGCATATCGTA
TCCACAGGCATCACGGCAGTGCTGCTCGTCTTGATTITTTGTTCTCAGAAAGAGAATAAAAT
GACAGTTGAGCTTTTCCAAATCACAAATAAAGCCATCAGCAGTGCTCCCTTCTCTGCTGTTC
AGCCACTGTGGACATTTGCCATCCTCATTTTCTTCTGGGCTCTCTGGGTGGCTGTGCTGTG
AGCCTGGGAACCTGCAGAGATGTCCTCCAGGTTATGGAAGCGCCGAAGTGGAAATATAGCCCT
TCTGGGCATTCGTGATCATGTGCTGATACCATTTAATTGGCCCTCATCTGGAATAGTGAATTCA
TTCTTGTGCTGCCACAATGACTATAGCTGGGGCAGTGTTACTTGTATTTCACAGAAAGT
AAAAATGATCCTCCTGATCATCCATCCTTTCGTCTCTCTCCATTCTCTCTCTTACCATCA
AGGAACCGTTGTGAAAGGTCATTTTTAATCTCTGTGGTGAGGATTCGAGAATCATTGTCA
TGTACATGCAAAACGCACTGAAAGAACAGCAGCATGGTGCAATTGTCCAGGTACCTGTTCCGA
TGCTGCTACTGCTGTTTCTGGTGTCTTGACAAATACCTGCTCCATCTCAACCAGAATGCATA
TACTACAACCTGCTATTAATGGGACAGATTTCTGTACATCAGCAAAAGATGCATTCAAATCT
TGTCCAAGAACTCAAGTCACTTTACATCTATTAAGTCTGTTGGAGACTTCATAATTTTCTA
GGAAAGGTGTTAGTGGTGTGTTTCACTGTTTGGAGGACTCATGGCTTTTAACTACAATCG
GGCATTCAGGTGTGGGCAGTCCCTCTGTTATTGGTAGCTTTTTTGCTACTTAGTAGCCC
ATAGTTTTTTATCTGTGTTTGAACCTGTGCTGGATGCATTTTCTCTGTGTTTGTGTTGAT
CTGGAACAAATGATGGATCGTCAGAAAAGCCCTACTTATGATCAAGAATTTCTGAGTT
CGTAAAAGGAGCAACAAATTAACCAATGCAAGGCCACAGCAGACAAGCACTCATTAAAGGA
ATGAGAGGGGAACCAAGATCCAGGCCATTGTGAGATAGATACCCATTAGGTATCTGTACCT
GGAAACCATTTTCTTCTAAGAGCCATTACAGAATTAGAAGATGAGACCACTAGAGAAAAGTT
AGTGAATTTTTTTTTTAAAGACCTAATAAACCCATTCTCTCTCAAAA

FIGURE 111

MSGRDTILGLCILALALSLAMMFTFRFITTTLLVHIFISLVILGLLFVCGVLWWLYDYDTNDL
SIELDTERENMKCVLGFIVSTGITAVLLVLIFVLRKRIKLTVELFQITNKAISSAPFLFQ
PLWTFAILIFFWVLWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWSYHLIGLIWTSEFI
LACQQMTIAGAVVTCYFNRSKNDPPDHPILSSLSILFFYHQGTVVKGSFLISVVRIPRIIVM
YMQNALKEQQHGALSRYLFRCCYCCFWCLDKYLLHLNQAYTTTAINGTDFCTSAKDAFKIL
SKNSSHFTSINCFGDFIIFLGKVLVVCFTVFGGLMAFNYNRAQVWAVPLLLVAFFAYLVAH
SFLSVFETVLDALFLCFAVDLETNDGSSEKPYFMDQEFLSFVKRSNKLNNARAQQDKHSLRN
EEGTELQAIVR

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FIGURE 112

GTTCGATTAGCTCCTCTGAGAAGAAGAGAAAAGGTTCTTGGACCTCTCCCTGTTTCTTCTCCTT
 AGAATAATTTGTATGGGATTTGTGATGCAGGAAAGCCTAAGGGAAAAAGAAATATTCATTCTCG
 TGTGGTGAAAATTTTGGAAAAAAATTTGCCCTTCTCAAACAAGGGGTGCATTCTGTATATTT
TATGAGGACTGTTGTTCTCACATGAAGGCATCTGTTATTGAAATGTTCTTGTGTTGCTGG
 TGACTGGAGTCAATTCAAACAAGAAACCGCAAGAAAGATTAAAGGCCCAAGTTCACCTGTTG
 CCTCAGATCAACTCGGATGTTCAAGCCGGGAAAGATCATCGATCCTCGAGTTCATTGTGAAATG
 TCCAGCAGGATGCCAAGACCCAAATACCATGTTTATGGCACTGACGTGTATGCATCCTACTT
 CCAGTCTGTTGGCGCTGCCGTACACAGTGGTGTGCTTGATAATTCAGGAGGGAAAAATACTT
 GTTCCGAAGGTTGCTGGACAGTCTGGTTACAAAGGGAGTTATTCACACGGTGTCCAATCGTT
 ATCCCTACCAGATGGAGAGAATCCTTTATCGTCTTAGAAAGTAAACCCAAAAAGGGGTGTAA
 CCTACCCATCAGCTCTTACATACTCATCATCGAAAAGTCCAGCTGCCAAGCAGGTGAGACC
 ACAAAGCCTATCAGAGGCCACCTATTCAGGGGACAACCTGCACAGCCGGTCACTCTGATGCA
 GCTTCTGGCTGTCACTGTAGCTGTGGCCACCCCAACCTTGCCAAAGGCCATCCCTCTCTG
 CTGCTTCTACCAACAGCATCCCCAGACCAATCAGTGGGCCACAGGAGCCAGGAGATGGAT
 CTCTGGTCCACTGCCACTACACAAGCAGCCAAAACAGGCCAGAGCTGATCCAGGTATCCA
 AAGGCAAGATCCTTCAGGAGCTGCCCTTCAGAAAACCTGTGGAGCGGATGTGACGCTGGGAC
 TTGTTCCAAAAGTGAATTTGAGCACACAGTCTTTGGAGCCAGTATCCCTGGGAGATCCAAAC
 TGCAAAATGACTTGTCTGTTTTTAATTTGATGGGAGCACCAGCATTGGCAACGGCGATTCCG
 AATCCAGAAGCAGCTCCTGGCTGATGTTGCCAAAGCTTTGACATTGGCCCTGCCGGTCCAC
 TSATGGTGTGTTGCCAGTATGGAGACAACCTGCTACTCACTTTAACTTCAAGACACACACG
 AATTTCTCGAGATCTGAAGACAGCCATAGAGAAAATTACTCAGAGAGGAGGACTTTCTAATGT
 AGGTCCGGCCATCTCCTTTGTGACCAAGAACTTCTTTCCAAAGCCAATGGAAACAGAGAGCG
 GGCTCCCAATGTGGTGGTGTGATGGTGGATGGCTGGCCACGGACAAAAGTGGAGGAGGCT
 TCAAGACTTGGCAGAGAGTCAGGAATCAACATTTTCTTCATCACCATTGAAGGTGCTGCTGA
 AATGAGAAGCAGTATGTGGTGGAGCCCAACTTTGCAACAAGGCCGTGTGCAGAACCAACG
 GCTTCTACTCGCTCCAGTGCAGAGCTGGTTTGGCCTCCACAAGACCTCTGCAGCTCTGGTG
 AAGCGGGTTCGCACTGACCGCTGCGCTGCGAGCAAGACCTGTTGAACCTCGGCTGACAT
 TGCTTCTGTCTCGACGGTCCAGCAGTGTGGGGACGGGCACTTCCGCAACCTGCTCCAGT
 TTGTGACCAACTACCAAGAGTTTGAGATTTCCGACACGGACACGCGCATCGGGGCCGTG
 CAGTACACCTACGAACAGCGGCTGGAGTTTGGTTTCGACAAGTACAGCAGCAAGCCTGACAT
 CCTCAACGCCATCAAGAGGGTGGGCTACTGGAGTGGTGGCACCAGCAGCGGGGCTGCCATCA
 ACTTCCGCCCTGGAGCAGCTCTTCAAGAGTCCAAGCCCAACAGAGGAAGTTAATGATCCTC
 ATCACCAGCGGAGGTCTTACGACGAGCTCCGGATCCCAAGCATGGCTGCCATCTGAAGGG
 AGTGAATCACTATGCGATAGGCGTTCGCTGGGCTGCCCAAGAGGAGCTAGAAGTCATTGCCA
 CTCAACCCGCGAGAGCACTCTCTTTTGTGGACGAGTTTGACAACCTCCATCAGTATGTC
 CCCAGGATCATCCAGAACATTTGTACAGAGTTCAACTCACAGCCTCGGAAGTGAATTCAGAG
 CAGGCAGCAGCCAGCAAGTGCTGCTTTACTTAAGTGACGTGTGGACACCCCAACCGCTTAA
 TGGGGCAGCCACGGTGCATCAAGTCTTTGGGCAGGGCATGGAGAAACAAATGCTCTGTTATTA
 TTTCTTGGCATCAGCTTTTTCATATTCAAAACCTTGGAGTTACAAAGATGATCAACAACGT
 ATAGAATGAGCCAAAAGGCTACATCATGTTGAGGGTGCTGGAGATTTTACATTTTGACAATT
 GTTTTCAAAAATAATGTTTCGGAATACAGTGCAGCCCTTACGACAGGCTTACGTAGAGCTTTT
 GTGAGATTTTTAAGTTGTTATTTCTGATTTGAACCTCTGTAACCTCAGCAAGTTTTCATTTT
 GTCATGACAATTAGGAATTTGCTGAATTAATGTTTGAAGGATGAAAAATAAAAA
 AA
 AA

FIGURE 113

MRTVVLTMKASVIEMFLVLLVTVGVHSNKETAKKIKRPKFTVPQINCVDKAGKIIDPEFIVKC
PAGCQDPKYHVYGTDVYASYSSVCGAHVHSGVLDNSGGKILVRKVAGQSGYKGSYSNGVQSL
SLPRWRESFIVLESKPKKGVTPSALTYSSSKSPAAQAGETTKAYQRPPPIPGTTAQPVVTLMQ
LLAVTVAVATPTTLPRPSPSAASTTSIPRPQSVGHRSEQEMDLWSTATYTSSQNRPRADPGIQ
RQDPSGAAFQKPVGADVSLGLVPKEELSTQSLEPVSLGDPNCKIDLSFLIDGSTSIGKRRFR
IQKQLLADVAQALDIGPAGPLMGVVQYGDNPATFNKLTHTNSRDLKTAIEKITQRGGLSNV
GRAISFVTKNFFSKANGNRSGAPNVVVVMVDGWPTDKVEEASRLARESGINIFFITIEGAAE
NEKQYVVEPNFANKAVCRTNGFYSLHVQSWFGLHKTLPVVKRVCDDRLACSKTCLNSADI
GFVIDGSSSVGTGNFRTVLQFVTNLTKEFEISDTDTRIGAVQYTYEQRLEFGFDKYSSKPDIL
LNAIKRVGYWGGTSTGAAINFALQLEFKKSKPNKRKLMILITDGRSYDDVRIPAMAAHLKG
VITYAIGVAWAAQEELEV IATHPARDHSFFVDEFDNLHQYVPRI IQNICTEFNSQPRN

FIGURE 114

CAGGATGAACTGGTTGCAGTGGCTGCTGCTGCTGCGGGGCGCTGAGAGGACACGAGCTCTA
TGCCCTTTCCGGCTGCTCATCCGCTCGGCCTCCTGTGCGCGCTGCTGCCTCAGCACCATGGT
 GCGCCAGGTCCCAGCGCTCCGCGCCAGATCCGCCCCACTACAGTTTTTCTCTGACTCTAAT
 TGATGCACTGGACACCTTGCTGATTTTGGGGAATGTCTCAGAATTCCAAAGAGTGGTTGAAG
 TGCTCCAGGACAGCGTGGACTTTGATATTGATGTGAACGCCCTCTGTGTTGAAACAAACATT
 CGAGTGGTAGGAGGACTCCTGTCTGCTCATCTGCTCTCCAAGAAGGCTGGGGTGGAAGTAGA
 GGCTGGATGGCCCTGTTCCGGGCTCTCCTGAGAATGGCTGAGGAGCGCGCCGAAACTCC
 TCCAGCCTTTCCAGACCCCACTGGCATGCCATATGGAACAGTGAACCTACTTCATGCGGTG
 AACCAGGAGAGACCCCTGTACCTGTACGGCAGGGATTGGGACCTTCATTGTTGAATTTGC
 CACCCTGAGCAGCCTCACTGGTGACCCGGTGTTCAAGATGTGGCCAGAGTGGCTTTGATGC
 GCCTCTGGGAGAGCCGGTCAGATATCGGGCTGGTCGGAACACATTGATGTGCTCACTGGC
 AAGTGGGTGGCCAGGACGAGGCATCGGGGCTGGCGTGGACTCCTACTTTGAGTACTTGGT
 GAAAGGAGCCATCCTGCTTCAGGATAAGAAGCTCATGGCCATGTTCTAGAGTATAACAAAG
 CCATCCGGAACACACCCGCTTCGATGACTGGTACCTGTGGGTTCAGATGTACAAGGGGACT
 GTGTCCATGCCAGTCTTCAGATCCTTGGAGGCCCTACTGGCCTGGTCTTCAGAGCCTCATTTG
 AGACATTGACAATGCCATGAGGACCTTCCTCAACTACTACACTGTATGGAAGCAGTTTGGGG
 GGCTCCCGGAATTCTACAACATTCTCAGGGATACACAGTGGAGAAGCGAGAGGGCTACCCA
 CTTGCGCCAGAACTTATTGAAAGCGCAATGTACCTCTACCGTGCCACGGGGGATCCCACCTT
 CCTAGAACTCGGAAGAGATGCTGTGGAATCCATTGAAAAATCAGCAAGGTGGAGTGC GGAT
 TTGCAACAATCAAAGATCTGCGAGACCACAAGCTGGACAACCGCATGGAGTCGTTCTTCTCTG
 GCCGAGACTGTGAAATACCTCTACCTCCTGTTTGACCCAACCAACTTCATCCACAACAATGG
 GTCCACCTTCGACGCGGTGATCACCCCTATGGGGAGTGCATCCTGGGGGCTGGGGGGTACA
 TCTTCAACACAGAAGCTCACCCCATCGACCTTGCCGCCCTGCACTGCTGCCAGAGGCTGAAG
 GAAGAGCAGTGGGAGGTGGAGGACTTGATGAGGGAATCTACTCTCTCAAACGGAGCAGGTC
 GAAATTTAGAAAAACATGTTAGTTCGGGGCCATGGGAACCTCCAGCAAGGCCAGGAACAC
 TCTTCTACCCAGAAAACCATGACCAGGCAAGGGAGAGGAAGCCTGCCAAACAGAAGGTCCCA
 CTTCTCAGCTGCCCCAGTCAGCCCTTCACTCCAAGTTGGCATTACTGGGACAGGTTTTCTCT
 AGACTCCTCATAACCACTGGATAATTTTTTATTTTTTATTTTTTTGAGGCTAACTATAATA
 AATTGCTTTTGGCTATCATAAAA

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FIGURE 115

MPFRLLIPLGLLCALLPQHHGAPGPDGSAPDPAHYSFSLTLIDALDTLLILGNVSEFQRVVE
VLQDSVDFDIDVNASVFETNIRVVGGLLSAHLLSKKAGVEVEAGWPCSGPLLRAEEEAARKL
LPAFQTPTGMPYGTVNLLHGVNPGETPVTCTAGIGTFIVEFATLSSLTGDPVVFEDVARVALM
RLWESRSDIGLVGNHIDVLTGKWVAQDAGIGAGVDSYFEYLVKGAILLQDKKLMAMFLEYNK
AIRNYTRFDDWYLVWQMYKGTVSMVPVFQSLEAYWPGQLQSLIGDIDNAMRTFLNYYTVWKQFG
GLPEFYNIPOGYTVEKREGYPLRPELIESAMYLYRATGDPPTLLELGRDAVESIEKISKVECG
FATIKDLRDHKLDRMESFFLAETVKYLYLLFDPTNFIHNNGSTFDAVITPYGECILGAGGY
IFNTEAHPIDLAALHCCQRLKEEQWEVEDLMREFYSLKRSRSKFQKNTVSSGPWEPPARPGT
LFSPENHDQARERKPAKQKVPLLSCPSQPFTSKLALLGQVFLDSS

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FIGURE 116

AAAGTTACATTTTCTCTGGAAGTCTCCTAGGCCACTCCCTGCTGATGCAACATCTGGGTTTG
 GGCAGAAAAGGAGGTGCTTCGGAGCCCGCCCTTTCTGAGCTTCTGGGCCGGCTCTAGAACA
 ATTACAGGCTTCGCTGCGACTCAGACCTCAGCTCCAACATATGCATTCTGAAGAAAGATGGCT
 GAGATGGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGTCAAACTGAGTCTACCA
AATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCTTTTCATGTGGTTTTTCT
 ACGCATTGATTCCATGTTTGGCTCACAGATGAAGTGGCCATTCTGCCTGCCCTCAGAACCTC
 TCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCAGTGATCGCGCTGGAGA
 AACAGTGTACTATTCTGTGCAATACCAGGGGGAGTACGAGAGCCTGTACACGAGCCACATCT
 GGATCCCCAGCAGCTGGTGTCTACTACTGAAGGTCTGAGTGTGATGTCACTGATGACATC
 ACGGCCACTGTGCCATACAACCTTCGTGTGAGGGCCACATTGGGCTCACAGACCTCAGCCTG
 GAGCATCCTGAAGCATCCCTTTAATAGAACTCAACCATCCTTACCCGACCTGGGATGGAGA
 TCACCAAAGATGGCTTCCACCTGGTTATTGAGCTGGAGGACCTGGGGCCCCAGTTTGAGTTC
 CTGTGTGGCCTACTGGAGGAGGGAGCCTGGTGCCGAGGAACATGTCAAATGGTGAGGAGTGG
 GGGTATTCCAGTGCACCTAGAAACCATTGGAGCCAGGGGCTGCATACTGTGTGAAGGCCAGA
 CATTCTGTGAAGGCCATTGGGAGGTACAGCGCCTTCAGCCAGACAGAATGTGTGGAGGTGCAA
 GGAGAGGCCATTCCCTGGTACTGGCCCTGTTTGCTTTGTTGGCTTCATGCTGATCCTTGT
 GGTGCTGCCACTGTTCTGTCTGGAAAATGGGCCGGCTGCTCCAGTACTCCTGTGCCCCGTGG
 TGGTCTCCAGACACCTTGAAAATAACCAATTACCCCGAGAAGTTAATCAGCTGCAGAAGG
 GAGGAGGTGGATGCCTGTGCCACGGCTGTGATGTCTCCTGAGGAACCTCCTCAGGGCCTGGAT
 CTCA**TAGG**TTTTGCGGAAGGGCCAGGTGAAGCCGAGAACCTGGTCTGCATGACATGGAACC
 ATGAGGGGACAAGTTGTGTTTTCTGTTTTCCGCCACGGACAAGGGATGAGAGAAGTAGGAAGA
 GCCTGTTGTCTACAAGTCTAGAAGCAACCATCAGAGGCAGGGTGGTTGTCTAACAGAACAC
 TGACTGAGGCTTAGGGATGTGACCTCTAGACTGGGGCTGCCACTTGCTGGCTGAGCAACC
 CTGGGAAAAGTGACTTCATCCCTTCGGTCTTAAGTTTTCTCATCTGTAATGGGGGAATTACC
 TACACACCTGCTAAACACACACACAGAGTCTCTCTATATATACACAGTACACATAAA
 TACACCCAGCACTTGAAGGCTAGAGGGAACTGGTGACACTCTACAGTCTGACTGATTACAG
 TGTTTCTGGAGAGCAGGACATAAATGTATGATGAGAATGATCAAGGACTCTACACACTGGGT
 GGCTTGGAGAGCCACTTTCCAGAAATAATCCTTGAGAGAAAAGGAATCATGGGAGCAATGG
 TGTTGAGTTCATTCAAGCCCAATGCCGGTGCAGAGGGGAATGGCTTAGCGAGCTCTACAGT
 AGGTGACCTGGAGGAAGGTACAGCCCACTGAAAATGGGATGTGCATGAACACGGAGGATC
 CATGAACACTGTAAAGTGTTGACAGTGTGTGCACACTGCAGACAGCAGGTGAAATGTTATGT
 GTGCAATGCGACGAGAATGCAGAAGTCAGTAACATGTGCATGTTTGTGTGCTCCTTTTTTC
 TGTGTGTAAGGTACAGAATTACGAAATAAAAAGGGCCACCTGGCCAAAAGCGGTAAAAAA
 AAAAAAAAAA

MQTFTMVLEEIWTSLFMWFFYALIPCLLTDEVAIPAPQNLSVLSTNMKHLMLMWSFVIAPGE
TVYYSVEYQGEYESLYTSHIWIWIPSSWCSLITEGPCDVTDDITATVPYNLVRATLHQSQSAW
SILKHFPFNRSNITILTRPGMEIKTDAIGHRLVLEIDLGPQFEFLVAYWRREPAAEEHVSMVS
GIPVHLETEMPGAAYCVKQAEFTVKAGFHSFASQSTCEVVEGEAIPLVALFAVFGFMILLV
VVPFLVWMKGRLLQYSCCPVVVLPTLKITINSFQKLISCRREEEDCATAVMSPEELLRAWIS

Signal peptide:

amino acids 1-29

amino acids 230-255

amino acids 40-43 and 134-137

Tissue factor proteins homology.

amino acids 92-119

Integrins alpha chain protein homology.

amino acids 232-262

FIGURE 118

TCCTGCTGATGCACATCTGGGTTTGGCAAAGGAGGTTGCTTCGAGCCGCCCTTTCTAGCTT
CCTGGCCGGCTCTAGAACAAATTCAGGCTTCGCTGCGACTAGACCTCAGCTCCAACATATGCA
TTCTGAAGAAAGATGGCTGAGATGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGG
TCAAACCTGAGTCTACCAAATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCT
TTTCATGTGGTTTTTTCTACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGC
CTGCCCCCTCAGAACCTCTCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCA
GTGATCGCGCCTGGAGAAACAGTGTACTATTCTGTGCAATACCAGGGGGAGTACGAGAGCCT
GTACACGAGCCACATCTGGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCCTGAGTGTG
ATGTCACTGATGACATCAGGCCACTGTGCCATACAACCTTTGTGTCAGGGCCACATTGGGC
TCACAGACCTCAGCCTGGAGCATCCTGAAGCATCCCTTTAATAGAAATCAACCATCCTTAC
CCGACCTGGGATGGAGATCACCAAAGATGGCTTNCACCTGGTTATTGAGCTGGAGGACCTGG
GGCCCCAGTTTGAGTTCCTTGTGGCCTANTGGAGGAGGGGCGAACCCCTTGCGGCGCAAGGG
GTTNGCGAACCCCTTGCGGCCGCTGGGGTATCTCTCGAGAAAAGAGAGGCCCAATATGACCCAC
ATACTCAATATGGACGAANTGCTATTGTCCACCTGTTTGAGTGGCGCTGGGTTGAT

FIGURE 119

CGGACGCGTGGGCCGCCACCTCCGGAACAAGCCATGGTGGCGGCGACGGTGGCAGCGGCGTG
 GCTGCTCCTGTGGGCTGCGGCCTGCGCGCAGCAGGAGCAGGACTTCTACGACTTCAAGGCGG
 TCAACATCCGGGGCAAACTGGTGTGCTGGAGAAGTACCGCGGATCGGTGTCCCTGGTGGTG
 AATGTGGCCAGCGAGTGGGCTTACAGACCAGCACTACCGAGCCCTGCAGCAGCTGCAGCG
 AGACCTGGGCCCCACCACCTTTAACGTGCTCGCCTTCCCCTGCAACCAGTTTGGCCAACAGG
 AGCCTGACAGCAACAAGGAGATTGAGAGCTTTGCCGCCGCACCTACAGTGTCTCATTCCCC
 ATGTTTAGCAAGATTGCAGTCACCGGTACTGGTGCCCATCCTGCCTTCAAGTACCTGGCCCA
 GACTTCTGGGAAGGAGCCACCTGGAACCTTCTGGAAGTACCTAGTAGCCCCAGATGGAAGG
 TGGTAGGGGCTTGGGACCCAACTGTGTCAGTGGAGGAGTGCAGCCCCAGATCACAGCGCTC
 GTGAGGAAGCTCATCTACTGAAGCGAGAAGACTTATTAACCACCGCGTCTCCTCCTCCACCA
 CCTCATCCGCCACCTGTGTGGGCTGACCAATGCAAACCTCAAATGGTGTCTCAAAGGGAG
 AGACCCACTGACTCTCCTTCCCTTACTCTTATGCCATTGGTCCCATCATTCTTGTGGGGGAA
 AAATTCTAGTATTTTGATTATTGAATCTTACAGCAACAAATAGGAACCTCGGCCAATGAG
 AGCTCTTGACCAGTGAATCACCAGCCGATACGAACGCTCTTGCCAACAAAAATGTGTGGCAA
 TAGAAGTATATCAAGCAATAATCTCCACCCAAAGGCTTCTGTAAACTGGGACCAATGATTAC
 CTCATAGGGCTGTTGTGAGGATTAGGATGAAATACCTGTGAAAGTGCCTAGGCAGTGCCAGC
 CAAATAGGAGGCATTCAATGAACATTTTTTGCATATAAAACCAAAAAATACTTGTTATCAAT
 AAAAACTTGCATCCAACATGAATTTCCAGCCGATGATAATCCAGGCCAAAGGTTTAGTTGTT
 GTTATTTCTCTGTATTATTTTCTTCATTACAAAAGAAATGCAAGTTCATTGTAACAATCCA
 AACAATACCTCAGGATATAAAATAAAATGAAAGTATCCTCCTCAAAA

FIGURE 120

MVAATVAAAWLLLWAAACAQQEQDFYDFKAVNIRGKLVSLVKYRGSVSLVVNVASECGFTDQ
HYRALQQQLQRDLGPHHFNVLAFFPCNQFGQQEPDSNKEIESFARRTYSVSFPMFSKIAVTGTG
AHPAFKYLAQTSKGKEPTWNFWKYLVPDGGKVVGAWDPTVSVVEEVRPQITALVRKLILLKREDL

FIGURE 121

CGGACGCGTGGGCGGGCCGGGACGCGAGGGCAAAGCGAGCC**ATG**GCTGTCTACGTCGGGATGC
 TGC GCCTGGGGAGGCTGTGCGCCGGGAGCTCGGGGGTGCTGGGGGCCCGGGCCGCCCTCTCT
 CGGAGTTGGCAGGAAGCCAGGTTGCAGGGTGTCGCCTTCTCAGTTCAGAGAGGTGGATCG
 CATGGTCTCCACGCCCATCGGAGGCCTCAGCTACGTTCAAGGGTGCACCAAAAAGCATCTTA
 ACAGCAAGACTGTGGGCCAGTGCCCTGGAGACCACAGCACAGAGGGTCCAGAACGAGAGGCC
 TTGGTGCCTCCATGAAGACGTAGGTTGACCTTTGCCAACTCAAGGAGGAGTGGACAA
 AGCTGCTTCTGGCCTCCTGAGCAATTGGCCTCTGCAAAGGTGACCGGCTGGGCATGTGGGAC
 CTAATCCTATGCATGGGTGCTCATGCAGTTGGCCACCGCCAGGCGGGCATCATCTGGTG
 TCTGTGAACCCAGCCTACCAGGCTATGGAACCTGGAGTATGCCTCAAGAAGGTGGGCTGCAA
 GGCCCTTGTTTCCCCAAGCAATTCAAGACCCAGCAATACTACAACGTCCTGAAGCAGATCT
 GTCCAGAAGTGGAGAATGCCAGCCAGGGGCCCTGAAGAGTCAGAGGCTCCCAGATCTGACC
 ACAGTCATCTCGGTGGATGCCCTTTGCCGGGGACCCCTGCTCCTGGATGAAGTGGTGGCGGC
 TGGCAGCACACGGCAGCATCTGGACCAGCTCCAATACAACAGCAGTTCCTGTCTGCCATG
 ACCCATCAACATCCAGTTACCTCGGGGACAACAGGCAGCCCCAAGGGGCCACCCCTCTCC
 CACTACAACATTTGTCAACAACTCCAACATTTTAGGAGAGCGCCTGAAACTGCATGAGAAGAC
 ACCAGAGCAGTTGCGGATGATCTGCCCAACCCCTGTACCATTGCCTGGGTTCCGTGGCAG
 GCACAATGATGTGCTGATGTACGGTGCCACCCCTCATCCTGGCCTCTCCCATCTTCAATGGC
 AAGAAGGCACCTGGAGGCCATCAGCAGAGAGAGAGGCACCTTCCTGTATGGTACCCCCACGAT
 GTTCGTGGACATTTCTGAACACGCCAGACTTCTCCAGTTATGACATCTCGACCATGTGTGGAG
 GTGTCAATTGCTGGGTCCCTTGCACTCCAGAGTTGATCCGAGCCATCATCAACAAGATAAAT
 ATGAAGGACCTGGTGGTTGCTTATGGAACCACAGAGAACAGTCCCGTGACATTCGCGCACTT
 CCTGAGGACACTGTGGAGCAGAAGGCAGAAAGCGTGGGCAGAAATTATGCCTCACACGGAGG
 CCCGGATCATGAACATGGAGGCAGGGACGCTGGCAAAGCTGAACAGCGCCGGGGAGCTGTGC
 ATCCGAGGGTACTGCGTCATGCTGGGCTACTGGGGTGAGCCTCAGAAGACAGAGGAAGCAGT
 GGATCAGGACAAGTGGTATTGGACAGGAGATGTGCCACAATGAATGAGCAGGGCTTCTGCA
 AGATCGTGGGCGCGCTCTAAGGATATGATCATCCGGGGTGGTGAGAACATCTACCCCGCAGAG
 CTCGAGGACTTCTTTACACACACCCGAAGGTGCAGGAAGTCAGGTTGGTGGGAGTGAAGGA
 CGATCGGATGGGGGAAGAGATTTGTGCCTGCATTCCGGCTGAAGGACGGGAGGAGACCACGG
 TGGAGGAGATAAAAGCTTTCTGCAAAGGGAAGATCTCTCACTTCAAGATTCCGAAGTACATC
 GTGTTTGTCAAACTACCCCTCACCATTTTCAGGAAGATCCAGAAATTCAAATTCGAGATC
 GCAGATGGAACGACATCTAAATCTG**TGA**ATAAAGCAGCAGGCGCTGTCTGGCCGGTTGGCTT
 GACTCTCTCCTGTGAGAATGCAACCTGGCTTTATGCACCTAGATGTCCCAGCACCAGTTTC
 TGAGCCAGGCACATCAATGTCAAGGAATTGACTGAACGAACCTAAGAGCTCCTGGATGGGT
 CGGGAACCTCGCCTGGGCACAAGGTGCCAAAAGGCAGGCAGCCTGCCAGGCCCTCCCTCCTG
 TCCATCCCCACATTCCTCTGTCTGTCTGTGATTTGGCATAAAGAGCTTCTGTTTTCTTT
 GAAAAAAAAAAAAAAAAA

FIGURE 122

MAVYVGMRLRLGRLCAGSSGVLGARAALSRWQEARLQGVRFLLSSREVD RMVSTPIGGLSYVQ
 GCTKKHLNSKTVGQCLETQARVPEREALVVLHEDVRLTFAQLKEEVDKAASGLLSIGLCKG
 DRLGMWGPNSYAWVLMQLATAQAGIILVSVNPAYQAMELEYVLKKVGCKALVFPKQFKTQQY
 YNVLKQICPEVENAQPGALKSQRLPDLTTVISVDAPLPGLLLDEVVAAAGSTRQHLDDQLQYN
 QQFLSCHDPINIQFTSGTTGSPKGATLSHYNIVNNSNILGERLKLHEKTPEQLRMILPNPLY
 HCLGSVAGTMMCLMYGATLILASPIFNGKKALEAISRERGTFLYGTPTMFVDILNQPDFSSY
 DISTMCGGVIAGSPAPPELIRAIINKINMKDLVAYGTTENSPTFAHFPEDTVEQKAESVG
 RIMPHTEARIMMEAGTLAKLNTPGELCIRGYCVMLGYWGEPEQKTEEAVDQDKWYWTGDVAT
 MNEQGFCIKIVGRSKDMIIRGENIYPAELEDFHHPKVQEVQVGVKDDRMGEEICACIRL
 KDGEETTVEEIKAFCKGKISHFKIPKYIVFVTNYPLTISGKIQKFKLREQMERHLNL

Signal Peptide:

amino acids 1-22

Transmembrane Domains:

amino acids 140-161, 213-229, 312-334

Putative AMP-binding Domain Signature:

amino acids 260-271

N-myristoylation Sites:

amino acids 19-24, 22-27, 120-125, 203-208, 268-273, 272-277,
 314-319, 318-323, 379-384, 380-385, 409-413

N-glycosylation Site:

amino acids 282-285

FIGURE 123

CAACTCCAACATTTTAGGAGAGCGCCTGAAACTGCATGAGAAGACACCAGAGCAGTTGCGGA
TGATCCTGCCCCAACCCCTGTACCATTGCCTGGGTTCCTGGCAGGCACAATGATGTGTCTG
ATGTACGGTGCCACCCCTCATCCTGGCCTCTCCCATCTTCAATGGCAAGAAGGCACTGGAGGC
CATCAGCAGAGAGAGAGGCACCTTCCTGTATGGTACCCCCACGATGTTCTGTGGACATTCTGA
ACCAGCCAGACTTCTCCAGTTATGACATCTCGACCATGTGTGGAGGTGTCATTGCTGGGTCC
CCTGCACCTCCAGAGTTGATCCGAGCCATCATCAACAAGATAAAATATGAAGGACCTGGTGGT
TGCTTATGGAACCACAGAGAACAGTCCCGTGACATTCGCGCACTTCCTGAGGACACTGTGG
AGCAGAAGGCAGAAAGCGTGGGCAGAATTATGCCTCACACGGAGGCGCGGATCATGAACATG
GAGGCAGGACGCTGGCAAAGCTGAACACGCCCGGGGAGCTGTGCATCCGAGGGTACTGCGT
CATGCTGGGCTACTGGGGTGAGCCTCAGAAGACAGAGGAAGCAGTGGATCAGGACAAGTGGT
ATTGGACAGGAGATGTCGCCAC

FIGURE 124

GAGCAGGACGGAGCC**ATG**ACCCCCGCCAGGAAAGCAGGTGCCAGGCCATGATCTGGACTGC
 AGGCTGGCTGCTGCTGCTGCTTCGCGGAGGAGCGCAGGCCCTGGAGTGCTACAGCTGCG
 TGCAGAAAGCAGATGACGGATGCTCCCCGAACAAGATGAAGACAGTGAAGTGCGCGCCGGGC
 GTGGACGTCTGCACCGAGGCCGTGGGGCGGTGGAGACCATCCACGGACAATTCTCGCTGGC
 AGTGCGGGGTTGCGGTTCTGGGACTCCCCGGCAAGAATGACCGCGGCCCTGGATCTTCAGGGGC
 TTCTGGCGTTTATCCAGCTGCAGCAATGCGCTCAGGATCGCTGCAACGCCAAGCTCAACCTC
 ACCTCGCGGGCGCTCGACCCGGCAGGTAATGAGAGTGATACCCGCCCAACGGCGTGGAGTG
 CTACAGCTGTGTGGGCTGAGCCGGGAGGCGTGCCAGGGTACATCGCCGCCGCTCGTGAGCT
 GCTACAACGCCAGCGATCATGTCTACAAGGGTGCTTCGACGGCAACGTCACCTTGACGGCA
 GCTAATGTGACTGTGTCTTGCTGTCCGGGGCTGTGTCCAGGATGAATTCTGCACTCGGGA
 TGGAGTAACAGGCCAGGGTTACGCTCAGTGGCTCCTGTTGCCAGGGGTCCCGCTGTAAT
 CTGACCTCCGCAACAAGACCTACTTCTCCCTCGAATCCCAACCCCTTGTCGGGCTGCCCCCT
 CCAGAGCCCACGACTGTGGCTCAACCACATCTGTCAACACTTCTACCTCGGCCCCAGTGAG
 ACCACATCCACCACCAACCATGCCAGCGCCAACAGTCAGACTCCGAGACAGGGAGTAG
 AACACGAGGCTCCCGGATGAGGAGCCAGGTTGACTGGAGGCGCCGCTGGCCACCAGGAC
 CGCAGCAATTCAGGGCAGTATCCTGCAAAAGGGGGCCCCAGCAGCCCCATAATAAGGCTG
 TGTGGCTCCACAGCTGGATTGGCAGCCCTTCTGTTGGCCGTGGCTGCTGGTGTCTACT**GT**
GAGCTTCTCCACCTGGAAATTTCCCTCTCACCTACTTCTCTGGCCCTGGGTACCCCTCTTCT
 CATCACTTCTGTGTTCCCACTGGACTGGGCTGGCCAGCCCTGTTTTCCAACATTCCC
 CAGTATCCCCAGCTTCTGCTGCGCTGTTTGGCGCTTTGGGAAATAAAATACCGTTGTATAT
 ATTTCTGCCAGGGGTGTTCTAGCTTTTTGAGGACAGCTCCTGTATCCTTCTCATCCTGTCTC
 TCCGCTTGCTCTTGTGTATGTTAGGACAGAGTGAGAGAAGTCAGCTGTACGGGGAAGGTG
 AGAGAGAGGATGCTAAGCTTCTACTCACTTTCTCCTAGCCAGCCTGGACTTTGGAGCGTGG
 GGTGGGTGGGACAATGGCTCCCCACTCTAAGCACTGCCTCCCTACTCCCGCATCTTGGG
 GAATCGGTTCCCATATGTCTTCCCTTACTAGACTGTGAGCTCCTCGAGGGGGGGCCCGGTAC
 CCAATTCGCCCTATAGTGAGTCGTA

FIGURE 125

MDPARKAGAAMIWTAGWLLLLLLRGGQALECYSCVQKADDGCSFNKMKTVKCAPGVDVCT
EAVGAVETIHGFSLAVRGCGSLPGKNDRGLDLHGLLAFTQLQCAQDRCAKLNLTSRAL
DPAGNESAYPPNGVECYSCVGLSREACQGTSPFVVCYNASDHVYKCFDGNVTLTAAANVTV
SLPVRGCVQDEFCTRDGVTGPGFTLSGSCCGSRCNSDLRNKTYFSRIPPLVRLPPPEPTT
VASTTSVTTSTSAFVRPTSTTKMPAPTSQTPRQGEHEASRDEEPRLTGGAAGHQDRSMSG
QYPAKGGPQQPHNKGCVAPTAGLAALLLAVAAGVLL

[illegible]

127/330

FIGURE 127

MELVLVFLCSLLAPMVLASAAEKEKEMDPFHYDYQTLRIGGLVFAVVLFSVGILLILSRCK
CSFNQKPRAPGDEEAQVENLITANATEPQKQRTevQPSGGSLWNLRRLLEPLDANVDA

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FIGURE 128

AAACTTGACGCCATGAAAGATCCCAGTCCTTCCTGCCGTGGTGCTCCTCTCCCTCCTGGTGCT
CCACTCTGCCCAGGGAGCCACCCTGGGTGGTCCTGAGGAAGAAAGCACCATTGAGAATTATG
CGTCACGACCCGAGGCCTTTAACACCCCGTTCTGAAACATCGACAAATTGCCGATCTGCGTTT
AAGGCTGATGAGTTCCTGAACTGGCACGCCCTCTTTGAGTCTATCAAAAGGAAACTTCCTTT
CCTCAACTGGGATGCCTTTCCTAAGCTGAAAGGACTGAGGAGCGCAACTCCTGATGCCCAGT
GACCATGACCTCCACTGGAAGAGGGGGCTAGCGTGAGCGCTGATTCTCAACCTACCATAACT
CTTTCCTGCCTCAGGAACTCCAATAAAACATTTCCATCCAAA

129/330

FIGURE 129

MKIPVLPAVVLLSLLVLHSAQGATLGGPEEESTIENYASRPEAFNTPFLNIDKLRSAPKADE
FLNWHALFESIKRKLPFLNWDAFPKLKGLRSATPDAQ

00991101.11101
101111.1011101

FIGURE 130

CAGTTCTGAAATCAATGGAGTTAATTTAGGGAATACAAACCAGCCATGGGGGTGGAGATTGC
CTTTGCCTCAGTGATTCTCACCTGCCTCTCCCTTCTGGCAGCAGGAGTCTCCAGGTTGTTT
TTCTCCAGCCAGTTCCAACTCAGGAGACAGGTCCCAAGGCCATGGGAGATCTCTCCTGTGGC
TTTGCCGGCCACTCATGAGAGTGTTTTTGTGTAAAGTATTTTTTAGAATACTGTTGACTTCT
TCATGATTTAATAACCATCCTTTGCGAAGTTTTATGAGGCTTTAGGGGAATGTCAACCCTCA
AATTTTTGTTATACTAGATGGCTTCCATTTACCCACCACCTATTTTAAGGTCCTTTATTTTT
AGGTTCAAGGTTCAATTTGACTTGAGAAAGTGCCTTCTGCAGCTTCATTGATTTTGTTTATC
TTCATAATTAATTGTAACGATTAAAAAGAATAAGAGCACGCAGACCTCTAGGAGAATATTT
TATCCCTGGGTGCCCCTGACACATTTATGTAGTGATCCACAAATGTGATTGTTAATTTAAA
TGTTATTCTAATATTAGTACATTCAGTTGTGATGTAATATGAATAACCAGAATCTATTTCTT
AAAAGTTTTGAGTATATTTTTCACTAGATATTTGTATAGAAAGACTGAATAGTGATG

131/330

FIGURE 131

MGVEIAFASVILTCLSLAAGVSQVLLQPVPQTQETGPKAMGDLSCGFAGHS

131/330

FIGURE 132

GGGGAATCTGCGATAGGTCTGCCGGCG**ATG**AGTGGTGGGCTAGCTCGCCGCTTCGGCTCTG
 GCTGCTGTTGTTCTCTGCCCTCAGCGCAGGGCCGCCAGAAGGAGTCAGGTTCAAAATGGA
 AAGTATTTATTGACCAAATTAACAGGTCTTTGGAGAATTACGAACCATGTTCAAGTCAAAAAC
 TGCAGCTGCTACCATGGTGTCTATAGAAGAGGATCTAACTCCTTTCCGAGGAGGCATCTCCAG
 GAAGATGATGGCAGAGGTAGTCAGACGGAAGCTAGGGACCCACTATCAGATCACTAAGAACA
 GACTGTACCGGGAAAAATGACTGCATGTTCCCTCAAGGTGTAGTGGTGTGAGCACTTTATT
 TTGGAAGTGATCGGGCGTCTCCCTGACATGGAGATGGTGATCAATGTACGAGATTATCCTCA
 GGTTCCCTAAATGGATGGAGCCTGCCATCCAGTCTTCTCCTTCAGTAAGACATCAGAGTACC
 ATGATATCATGTATCCTGCTTGGACATTTTGGGAAGGGGGACCTGCTGTTTGCCAATTTAT
 CCTACAGGTCTTGGACGGTGGGACCTCTTCAGAGAAGATCTGGTAAGGTCAGCAGCACAGTG
 GCCATGGAAAAAGAAAACTCTACAGCATATTTCCGAGGATCAAGGACAAGTCAGAACGAG
 ATCCTCTCATTTCTGTCTCGGAAAAACCCAAAACCTGTTGATGCAGAAATACACCAAAAAAC
 CAGGCCCTGGAATCTATGAAAGATACCTTAGGAAAGCCAGCTGCTAAGGATGTCCATCTTGT
 GGATCACTGCAATACAGTATCTGTTTAATTTTCGAGGCGTAGCTGCAAGTTTCCGGTTTA
 AACACCTCTTCTGTGTGGCTCACTTGTTTTCCATGTTGGTGATGAGTGGCTAGAATTCTCT
 TATCCACAGCTGAAGCCATGGGTTCACTATATCCAGTCAAAACAGATCTCTCCAATGTCCA
 AGAGCTGTTACAATTTGTAAGCAAATGATGATGTAGCTCAAGAGATTGCTGAAAGGGGAA
 GCCAGTTTATTAGGAACCATTTGCAGATGGATGACATCACCTGTTACTGGGAGAACCTCTTG
 AGTGAATACTCTAAATTCCTGTCTTATAATGTAACGAGAAGGAAAGGTTATGATCAAATTAT
 TCCCAAATGTTGAAACTGAAC**TAG**TAGTCATCATAGGACCATAGTCCTCTTTGTGGCA
 ACAGATCTCAGATATCCTACGGTGAGAAGCTTACCATAAGCTTGGCTCCTATACCTTGAATA
 TCTGCTATCAAGCCAAATACCTGGTTTTCTTATCATGCTGCACCAGAGCAACTCTTGAGA
 AAGATTTAAATGTGTCTAATACACTGATATGAAGCAGTTCAACTTTTGGATGAATAAGGA
 CCAGAAATCGTGAGATGTGGATTTTGAACCAACTCTACCTTTCATTTTCTTAAGACCAATC
 ACAGCTTGTGCCCTCAGATCATCCACCTGTGTGAGTCCATCACTGTGAAATTGACTGTGTCCA
 TGTGATGATGCCCTTTGTCCATTATTTGGAGCAGAAAAATTCGTCAATTTGGAAGTAGTACAA
 CTCATTGCTGGAATTGTGAAATATTCAAGGCGTGATCTCTGTCACTTTATTTTAATGTAGG
 AAACCCATATGGGGTTTATGAAAAATACTTGGGGATCATCTCTGAATGGTCTAAGGAAGCGG
 TAGCCATGCCATGCAATGATGTAGGAGTTCTCTTTGTAAAACCATAACTCTGTACTCAG
 GAGGTTTCTATAATGCCACATAGAAAGAGGCCAATTGCATGAGTAATTATTGCAATTGGATT
 TCAGGTTCCCTTTTGTGCCCTCATGCCCTACTTCTTAATGCCTCTCTAAAGCCAAA

FIGURE 133

MEWWASSPLRLWLLLFLLPSAQGRQKESGSKWKVFIDQINRSLENYEPCSSQNCSCYHGVIE
EDLTPFRGGISRKMMAEVVRRKLGTHYQITKNRLYRENDCMFPSRCSGVEHFILEVIGRLPD
MEMVINVRDYPQVPKWMEPAIPVFSFSKTSEYHDIMYPAWTFWEGGPAVWPYIPTGLGRWDL
FREDLVRSAAQWPWKKKNSTAYFRGSRTSPERDPLILLSRKPNKLVDAEYTKNQAWKSMKDT
LGKPAAKDVHLVDHCKYKYLFRGVAASFRFKHLFLCGSLVFHVGDWLEFFYPQLKPWWH
YIPVKTDLSNVQELLQFVKANDDVAQEIAERGSQFIRNHLQDDITCYWENLLSEYSKFLSY
NVTRRKGYDQIIPKMLKTEL

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FIGURE 134

CACCCCTCCATTCTCGCCATGCCCCCTGCAGCTGCTCCTGATCCCTGCTGCCCTCGCCTCTT
 TCATCCTGGCCTTTGGCACCGGAGTGGAGTTCGTGCGCTTTACCTCCCTTCGGCCACTTCTT
 GGAGGGATCCCGAGTCTGGTGGTCCGGATGCCCGCCAGGGATGGCTGGCTGCCCTGCAGGA
 CCGCAGCATCCTTGCCCCCTGGCATGGGATCTGGGGCTCCTGCTTCTATTGTGGGCAGC
 ACAGCCTCATGGCAGCTGAAAGAGTGAAGGCATGGACATCCCGGTACTTTGGGGTCTTCAG
 AGGTCACTGTATGTGGCTGCACTGCCCTGGCCTTGACAGTGGTGATGCGGTACTGGGAGCC
 CATACCCAAAGGCCCTGTGTTGTGGGAGGCTCGGGCTGAGCCATGGGCCACCTGGGTGCCGC
 TCCTCTGCTTTGTGCTCCATGTCACTCCTGGCTCCTCATCTTTAGCATCCTTCTGCTCTTT
 GACTATGCTGAGCTCATGGGCCTCAAACAGGTATACTACCATGTGCTGGGGCTGGGCGAGCC
 TCTGGCCCTGAAGTCTCCCCGGGCTCTCAGACTCTTCTCCACCTGCGCCACCCAGTGTGTG
 TGGAGCTGCTGACAGTCTGTGGTGGTGCCTACCTGGGCACGACCGTCTCCTCCTTGCT
 TTCCTCCTTACCCTCTACCTGGGCCTGGCTCAGGGCTTGATCAGCAAGACCTCCGCTACCT
 CCGGGCCAGCTACAAAGAAAACCTCCACCTGCTCTCTCGGCCCCAGGATGGGGAGGCAGAGT
GAGGAGCTCACTCTGGTTACAAGCCCTGTTCTTCTCCTCTCCCACTGAATTCTAAATCCTTAAC
 ATCCAGGCCCTGGCTGCTTCATGCCAGAGGCCAAATCCATGGACTGAAGGAGATGCCCTT
 CTACTACTTGAGACTTTATTCTCTGGGTCCAGCTCCATACCTAAATTCTGAGTTTCAGCCA
 CTGAACCTCAAGGTCCACTTCTCACCAGCAAGGAAGAGTGGGGTATGGAAGTCATCTGTCCC
 TTCACTGTTTAGAGCATGACACTCTCCCCCTCAACAGCCTCCTGAGAAGGAAAGGATCTGCC
 CTGACCACTCCCCTGGCACTGTTACTTGCCCTCTGCGCCTCAGGGGTCCCCCTTCTGACCGCT
 GGCTTCCACTCCAAGAAGGTGGACCAGGGTCTGCAAGTTCAACGGTCATAGCTGTCCCTCCA
 GGCCCCAACCTTGCTCACCCTCCCGGCCCTAGTCTCTGCACCTCCCTTAGGCCCTGCCTCT
 GGGCTCAGACCCCAACCTAGTCAAGGGGATTCTCCTGCTCTTAACTCGATGACTTGGGGCTC
 CCTGCTCTCCCGAGGAAGATGCTCTGCAGGAAAATAAAAGTCAGCCTTTTTTCTAAAAAAA

FIGURE 135

MAPALLLIPAAALASFILAFGTGVEFVRFSTSLRPLLGGIPESGGPDARQGWLAAALQDRSILAP
LAWDLGLLLLFVGQHSLSMAAERVKAWTSRYFGVLQRSLYVACTALALQLVMRYWEPKPGPV
LWEARAEPWATWVPLLCFVLHVISWLLIFSILLVFDYAEMLGLKQVYYHVLGLGEPLALKSP
RALRLFSHLRHPVCVELLTVLWVPTLTGDRLLLAFLLTLYLGLAHGLDQQDLRYLRAQLQR
KLHLLSRPQDGEAE

Signal sequence:

amino acids 1-13

Transmembrane domains:

amino acids 58-76, 99-113, 141-159, 203-222

N-myristoylation sites:

amino acids 37-43, 42-48, 229-235

099131-11501

FIGURE 136

CCGAGCACAGGAGATTGCTGCGTTTAGGAGGTGGCTGCGTTGTGGGAAAAGCTATCAAGGA
 AGAAATTGCCAAACCATGTCTTTTTTCTGTTTTTCAGAGTAGTTTCACAACAGATCTGAGTGT
 TTTAATTAAGCATGGAATACAGAAAAACAACAAAAAAGCTTAAGCTTTAATTTTCATCTGGAATT
 CCACAGTTTTCTTAGCTCCCTGGACCCGGTTGACCTGTTGGCTCTTCCCGCTGGCTGCTCTA
 TCACGTGGTGCTCTCCGACTACTCACCCGAGTGTAAAGAACCTTCGGCTCGCGTGCTTCTG
 AGCTGCTGTGGATGCTCGGCTCTCTGGACTGTCTTCCGAGTAGGATGTCACTGAGATCC
 CTCAAATGGAGCCTCCTGCTGCTGTCACTCCTGAGTTTCTTTGTGATGTGGTACCTCAGCCT
 TCCCCACTACAATGTGATAGAACGCGTGAAGTGGATGTACTTCTATGAGTATGAGCCGATTT
 ACAGACAAGACTTTCACTTCACACTTCGAGAGCATTCAAAGTCTCTCATCAAAATCCATTT
 CTGGTCACTTCTGGTGACCTCCACCCCTTCAGATGTGAAAGCCAGGCAGGCCATTAGAGTTAC
 TTGGGGTGAAAAAAGTCTTGGTGGGGATATGAGGTTCTTACATTTTCTTATTAGGCCAAG
 AGGCTGAAAAGGAAGACAAAATGTTGGCATTGTCTTAGAGGATGAACACCTTCTTTATGGT
 GACATAATCCGACAAGATTTTTTAGACACATATAATAACCTGACCTTGAAAACCATTTATGGC
 ATTCAGGTGGGTAAGTGTGTTTTGCCCAATGCCAAGTACGTAATGAAGACAGACACTGATG
 TTTTCATCAATACTGGCAATTTAGTGAAGTATCTTTAAACCTAAACCACTCAGAGAAGTTT
 TTCACAGGTATCCTCTAATTGATAATTATTCCTATAGAGGATTTTACCAAAAAACCCATAT
 TTCTTACCAGGAGTATCCTTTCAAGTGTTCCCTCCATACTGCAGTGGGTGGGTGTATATAA
 TGTCAGAGATTTGGTGCCAAGGATCTATGAAATGATGGGTACGTAAAACCCATCAAGTTT
 GAAGATGTTTATGTCGGGATCTGTTGAATTTATTAAGAGTGAACATTCTATTTCCAGAAGA
 CACAAATCTTTTCTTCTATATAGAATCCATTTGGATGTCTGTCAACTGAGACGTGTGATTG
 CAGCCCCATGGCTTTTCTTCCAAGGAGATCATCACTTTTGGCAGGTCATGCTAAGGAACACC
 ACATGCCATTATTAACCTTCACATTCTACAAAAAGCCTAGAAGGACAGGATACCTTGTGGAAA
 GTGTTAAATAAAGTAGGTACTGTGGAATAATTCATGGGAGGTGAGTGTGCTGGCTTCACTG
 AACTGAAACTCATGAAAAACCCAGACTGGAGACTGGAGGGTTACACTTGTGATTATTAGTC
 AGGCCCTTCAAAGATGATATGTGGAGGAATTAATATAAAGGAATTTGAGGTTTTTGTGTA
 GAAATTAATAGGACCAACAATTTGGACATGTCATTCTGTAGACTAGAATTTCTTAAAGGG
 TGTTACTGAGTTATAAGCTCACTAGGCTGTAAAAACAAACAATGTAGAGTTTTATTTATTG
 AACAAATGTAGTCACTTGAAGGTTTTGTGTATATCTTATGTGGATTACCAATTTAAAAATATA
 TGTAGTTCTGTGTCAAAAAACCTTCTTCACTGAAGTTATACTGAACAAAATTTTACCTGTTTT
 TGGTCATTTATAAAGTACTTCAAGATGTGACGATTTTACAGTTATTATTATTTAAATTA
 CTTCAACTTTGTGTTTTTAAATGTTTTGACGATTTCAATACAAGATAAAAGGATAGTGAAT
 CATTCCTTACATGCAACATTTTCCAGTTACTTAACTGATCAGTTTATTATTGATACATCAC
 TCCATTAATGTAAGTCATAGGTCATTATTGCATATCAGTAATCTCTTGGACTTTGTTAAAT
 ATTTTACTGTGGTAAATATAGAGAAGAATTAAGCAAGAAAACTGAAAA

FIGURE 137

MASALWTVLPSRMSLRSLKWSLLLLLSLSSFVMWYLSLPHYNVIERVNWMYFYEYEPiYRQD
FHFTLREHSNCSHQNPFVLVILVTSHPSDVKARQAIRVTWGEKKSWWGYEVLTFLLGQEA EK
EDKMLALSLEDEHLLYGDIIRQDFLDTYNNLT LKTIMAFRWVTEFCPNAKYVMKTD TDVFIN
TGNLVKYLNLNLNHSEKFFTGYPLIDNYSYRGFYQKTHISYQEYPFKVFPPYCSGLGYIMSRD
LVPRIYEMMGHV KPIKFEDVYVGICLNLLKVN IHI PEDTNLFFLYRIHLDVCQLRRVIAAHG
FSSKEIITFWQVMLRNTTCHY

000110111001

FIGURE 138

CCTCTGTCCACTGCTTTCGTGAAGACAAGATGAAGTTCACAATTGTCTTTGCTGGACTTCTT
GGAGTCTTTCTAGCTCCTGCCCTAGCTAACTATAATATCAACGTCAATGATGACAACAACAA
TGCTGGAAGTGGGCAGCAGTCAGTGAGTGTCAACAATGAACACAATGTGGCCAATGTTGACA
ATAACAACGGATGGGACTCCTGGAATTCCATCTGGGATTATGGAAATGGCTTTGCTGCAACC
AGACTCTTTCAAAGAAGACATGCATTGTGCACAAAATGAACAAGGAAGTCATGCCCTCCAT
TCAATCCCTTGATGCACTGGTCAAGGAAAAGAAGCTTCAGGGTAAGGGACCAGGAGGACCAC
CTCCAAGGGCCTGATGTACTCAGTCAACCCAAACAAAGTCGATGACCTGAGCAAGTTCGGA
AAAAACATTGCAAACATGTGTCGTGGGATTCCAACATACATGGCTGAGGAGATGCAAGAGGC
AAGCCTGTTTTTTTACTCAGGAACGTGCTACACGACCAGTGACTATGGATTGTGGACATTT
CCTTCTGTGGAGACACGTGGAGAACTAAACAATTTTTTAAAGCCACTATGGATTTAGTCAT
CTGAATATGCTGTGCAGAAAAAATATGGGCTCCAGTGGTTTTTACCATGTCATTCTGAAATT
TTTCTCTACTAGTTATGTTTGATTCTTTAAGTTTCAATAAAATCATTTAGCATTGAAAAAAA

FIGURE 139

MKFTTIVFAGLLGVFLAPALANYNINVNDDNNNAGSGQQSVSVNNEHNVANVDNNGWDSWNS
IWDYGNNGFAATRLFQKKTCIVHKMNKEVMPSTQSLDALVKEKKLQGKGPGGPPPKGLMYSVN
PNKVDDLKFKGNIANMCRGIPTYMAEEMQEASLFFYSGTCYTTSVLWIVDISFCGDTVEN

Signal Peptide:

amino acids 1-20

N-myristoylation Sites:

amino acids 67-72, 118-123, 163-168

Flavodoxin protein homology:

amino acids 156-174

CATTCTCTGAAACTAATCGTGTGCAGAAATTGACTTTGAAAAGCATTGCTTTTTACAGAAGTATTA
TTAACTTTTTTAGGAGTAATTTCTAGTTTGGATTGTAATATGAAATAATTTAAAAGGGCTTCG
CTCATATATAGGAAAATCGCATATGGTCTAGTATTAAATTCCTATTGCTTACTGATTTTTT
TGAGTTAAGAGTTGTTATATGCTAGAATATGAGGATGTGAATATAAATAAGAGAAGAAAAA
GAATAAAGTAGATTGAGTCTCCAATTTTATGTAAAGCTTCAGAAGAACTGGTTTGTTACATG
CAAGCTTATAGTTGAAATATTTTTTCAGGAATTACATGAATTGACAGTCTTCGAACCAATGTGT
TTGTTTCGATTTCAACCAGAGACTATAGCATGTGCTTGCATCTACCTTGCAGCTAGAGCACTT
CAGATTCGGTGGCAACTCGTCCCAATTGGTTTCTTCTTTTTGGTACTACAGAAGAGGAAAT
CCAGGAAATCTGCATAGAAACACTTAGGCTTTTATACCAGAAAAAGCCAAACTATGAATTAC
TGGAAAAAGAAGTAGAAAAAGAAAAAGTAGCCCTTACAAGAAGCCAAATTTAAAGCAAAGGGA
TTGAATCCGGATGGAACCTCAGCCCTTTCAACCCCTGGGTGGATTTTCTCCAGCTCCAAGCC
ATCATCAACCAAGAGAAGTAAAAGCTGAAGAGAATAACCAACTCTCCATTAATGTGAAGACAG
TCAAAAAAGAACCTGAGGATAGACAACAGGCTTCCAAGCCCTTACAATGGTGTAAAGAAA
GACAGCAAGAGAAGTAGAAATAGCAGAAGTGCAAGTCGATCGAGGTCAAGAACACGATCACG
TTCTAGATCACATACTCCAAGAAGACACTATAATAATAGGCGGAGTCGATCTGGAACATACA
GCTCGAGATCAAGAAGCAGGTCCCGCAGTCACAGTGAAGGCCCTCGAAGACATCATAATCAT
GGTCTCCTCACCTTAAGGCCAAGCATACCAGAGATGATTTAAAAGTTCAAACAGACATGG
TCATAAAAGGAAAAAATCTCGTTCTCGATCTCAGAGCAAGTCTCGGGATCACTCAGATGCAG
CCAAGAAACACAGGCATGAAAGGGGACATCATAGGGACAGGCGTGAACGATCTCGCTCCTTT
GAGAGGTCCCATAAAGCAAGACCATTGGTGGCAGTCGCTCAGGACATGGCAGGCACAGGCG
CTGACTTTCTCTTCCTTTGAGCCTGCATCAGTTCCTTGTTTTGCCTATCTACAGTGTGATGT
ATGGACTCAATCAAAAACATTAAACGCCAACTGATTAGGATTTGATTTCTTGAAACCCTCTA
GGTCTCTAGAACACTGAGGACAGTTTCTTTTGAAAAGAACTATGTTAATTTTTTGCACATT
AAAATGCCCTAGCAGTATCTAATTA AAAACCATGGTCAGGTTCAATTGTACTTTATTATAGT
TGTGTATTGTTTATTGCTATAAGAAGCTGGAGCTGAATTCGTAAAAATGTATCTTATTTT
ATACAGATAAAAATTGCAGACATGTTCTATTTAAGTGGTTATTGTTTAAATGATGGTGAAT
ACTTCTTTAACACTGGTTTGTCTGCATGTGTTAAAGATTTTACAAGGAAATAAAATACAAAT
CTTGTTTTTTTTCTAAAAAAAAAAAAAAAGT

141/330

FIGURE 141

MNDSLRTNVFVRFPETIACACIYLAARALQIPLPTRPHWFLFLFGTTEEEIQEICIETLRLY
TRKKPNYELLEKEVEKRVKALQEAQKAKGLNPDGTPALSTLGGFSPASKPSSPREVKAEK
SPISINVKTVKKEPEDRQQASKSPYNGVRKDSKRSRNSRSASRSRSRTRSRSRSHTPRRHYN
NRRSRSGTYSSRSRSRSHSESPRRHNNHGSPHLKAKHTRDDLKSSNRHGHKRKKSRSRSQ
SKSRDHSDAKKHRHERGHHRDRRERSRSFERSHKSXHHGGSRSGHGRHR

0999181.111501

FIGURE 142

TGGGGATAAAGGAAAAATGGTCAGGTATTAATGGCTTAAAGATTATTGGAAGGGGTTTATCA
TTTTTTGAANNNTATTCGGGTCANAATTGNCTTTGAAAAGCATTGCTTTTTACAGAAATATAT
TANCTTTTATAGAGTAATTCTAGTTTGGATTGTAATATGAAATTATTTAAAAGGGCTTCGCT
CATATATAGGAAAATCGCATATGGTCCTAGTATTAATTTNTTATTGCTTACTGATTTTTTTG
AGTTAAGAGTTGTTATATGNTAGAATATGAGGATGTGAATATAAATAAGAGAAGAAAAAGA
ATAAAGTAGATTGAGTCTCCAATTTTATGTAAGCTTCAGAAGAACTGGTTTGTTTACATGCA
AGCTTATAGTTGAAATATTTTTTCAGGAATTACATGAATGACAGTCTTCGAACCAATGTGTTT
GTTTCGATTTCAACCAGAGANTATAGCATGTGCTTGCATCTACCTTGCAGNTAGAGCACTTCA
GATTCCGTTGCCAACTNGTCCCATTTGGTTTCTTCTTTTTTGGTACTACAGAAGAGGAAATCC
AGGAAATNTGCATAGAAACACTTAGGCTTTATACCAGAAAAAGCCAACTATGAATTACTG
GAAAAAGAAGTAGAAAAAGAAAAGTAGCCTTACAAGAAGCCNAATTAAAAGCAAAGGGATT
GAATCCGGATGGAATCCAGCCCTTCAACCCTGGGTGGATTCTCTCC

FIGURE 144

MAVLGVQLVVTLLTATLMHRLAPHCSFARWLLCNGSLFRYKHPSEELRALAGKPRPRGRKE
RWANGLSEKPLSVPRDAPFQLETCPLTTVDALVLRFFLEYQWFVDFAVYSGGVYLFTEAYY
YMLGPAKETNIAVFWCLLTVTFSIKMFLTVTRLYFSAEEGERSVCLTFAFLFLLAMLVQV
VREETLELGLEPGLASMTQNLEPLLKKQGDWALPVAKLAIRVGLAVVGSVLGAFLTFFGLR
LAQTHRDALTMSEDRPMLQFLLHTSFLSPLFILWLWTKPIARDFLHQPPFGETRFSLLSDSA
FDSGRLWLLVVLCLLRLAVTRPHLQAYLCLAKARVEQLRREAGRIEAREIQQRVVVRYCYVT
VVSLOYLTPLILTLNCTLLKTLGGYSWGLGPAPLLSPDPSSASAAPIGSGEDEVQQTAARI
AGALGGLLTPLFLRGVLAYLIWWTAACQLLASLFGLYFQHLAGS

144/330

FIGURE 145

CGTTNGCAGCGTCAATGGCGGTCCTCGGAGTACAGCTGGTGGTGACCCTGCTCACTGCCAC
CCTCATGCACAGGCTGGCGCCACACTGCTCCTTCGCGCGCTGGCTGCTCTGTAACGGCAGTT
TGTTCCGATACAAGCACCCGNTTGGAGGAGGAGCTTCGGGCCCTGGCGGGGAAGCCGAGGCC
CAGAGGCAGGAAAAGAGCGGTGGGCCAATGGCCTTAGTGAGGAGAAGCCACTGTCTGTGCCCC
GAGATGCCCCGTTCAGCTGGAGACCTGCCCCCTCACGACCGTGGATGCCCTGGTCCTGCGC
TTCTTCCTGGAGTACCAGTGGTTTGTGGACTTTGCTGTGTACTCGGGCGCGTGTACCTCTT
CACAGAGGCCTACTACTACATGCTGGGACCAGCCAAGGAGACTAACATTGCTGTGTCTGGT
GCCTGCTCACAGTGACCTTCTCCATCAAGATGTTCTGACAGTGACACGGCTGTACTTCAGC
GCCGAGGAGGGGGGTGAGCGCTCTGTCTGCCTCACCTTGGCCTTCTCTCTGCTGCTGGC
CATGCTGGTGCAAGCG

FIGURE 146

GGTTCCTACATCCCTCATCTGAGAATCAGAGAGCATAACTTCTTACGGGCCCGTGATTATTAAACGTGGCTT
 AATCTGAAGGTTCTCAGTCAAAATCTTTGTGATCTACTGATTGTGGGGGCATGGCAAGGTTTGCTTAAAGGAGG
 TTGGCTTGGTTTGGGCCCTTGTAGCTGACAGAAGGTGGCCAGGGAGAATGCAGCACACTGCTCGGAGAATAAGG
 CGCTCTGTGCTGGTCTTGGCCTTGGCTCAGTCTTGCTAACTACATTGACAAATGTGGGCAACCTGCACCTTCTCTG
 TATTCAAGACTCTTAAAGGTGCCTCCACTACGGCCTGACCAAAGATAGGAAGAGGCGCTCAACAAGATGGCTG
 TCCAGACGCGTGTGGAGCCTCAGAGCCACGGCTCCCTCCCCAGAGGTTTCTGCAGCTGCCACCATCTCCTTAA
 TGACAGACGAGCCTGGCCTAGACAAACCTGCCTACGTGTCTCGGCAGAGGACGGGCAGCCAGCAATCAGCCCA
 GTGGACTCTGGCCGGGAGCAACCGAACTAGGCCACGGCCCTTGGAGAGATCCACTATTAGAAGCAGATCATTTAA
 AAAAATAAATCGAGCTTTGAGTGTTCTTCGAAGGACAAGAGCGGGAGTGCAGTTGCCAACCATCCGACACAGG
 GCAGGGAAAATTCTGAAAACCCACTGCCCTGAAGTCTTTCCAAAGTTGTACCACTGATTCCAGATGGTGAA
 ATTACCAGCATCAAGATCAATCGAGTAGATCCAGTGAAAGCCTCTCTATTAGGCTGGTGGGAGGTAGCGAAAC
 CCCACTGGTCCATATCATTATCCAACACATTTATCGTGATGGGGTGATCGCCAGAGACGGCCGGCTACTGCCAG
 GAGACATCATCTAAAGGTCAACGGGATGGACATCAGCAATGTCCCTCACAACACGCTGTGCGCTCTCCTGGCGG
 CAGCCCTGCCAGGTGCTGTGGCTGACTGTGATGCGTGAACAGAAGTTCCGAGCAGGAACAATGGACAGGCCCC
 GGTATGCTACAGACCCCGAGATGACAGCTTTTCATGTGATTCTCAACAAAAGTAGCCCCGAGGAGCAGCTTGGAA
 TAAAACTGGTGCAGAGTGGATGAGCCTGGGTTTTTCATCTTCAATGTGCTGGATGGCGCTGTGGCATATCGA
 CATGCTCAGCTTGAGGAGAATGACCGTGTGTAGCCATCAATGGACATGATCTTCGATATGGCAGCCAGAAAG
 TGGCGCTCATCTGATTGAGGCCAGTGAAGACGTGTTCACTCGTGTGCCCGAGGTTGGGCAGCGGAGCC
 CTGACATCTTTGAGGAAGCCGGCTGGAACAGCAATGGCAGCTGGTCCCCAGGGCCAGGGGAGAGGAGCAACT
 CCCAAGCCCCCTCCATCCTACAATTACTTGTGCATGAGAAGTGGTAAATATCCAAAAGACCCCGAGCTCTCT
 CGGCATGACCGTCGACGGGGGAGCATCACATAGAGAAATGGGATTGCGCTATCTATGTCACTAGTGTGAGCCCG
 GAGGAGTCATAAGCAGAGATGGAAGAATAAAAAACAGGTGACATTTTGTGAATGTGGATGGGGTCGAAGTGACA
 GAGGTGAGCCGAGTGGGCGAGTGGCATTATTGAAAGAACATCATCTCGATAGTACTCAAGACTTTGGAAGT
 CAAAGAGTATGAGCCCGAGGAAGACTGCAGCAGCCAGCAGCCCTGGACTCCAACCAACATGGCCCCACCCA
 GTGACTGGTCCCCATCTCGGTTCATGTGGCTGGAAATACACCGTGCTTGTATAACTGTAAAGATATTGTATTA
 CGAAGAAACACAGCTGGAAGTCTGGGCTTCTGCATTGTAGGAGGTTATGAAGAATACAATGGAAACAAACCTTT
 TTTTCATCAATCCATTTGTTGAAGGAACACAGCATACAATGATGGAAGAATAGATGGTGATATTCTTCTTG
 CTGTCAATGGTGAAGTACATCAGGAATGATACATGCTTGTGGCAAGACTGCTGAAAGAACTTAAAGGAAGA
 ATTACTCTAACTATTGTTTCTGGCCTGGCACTTTTTTATAGAAATCAATGATGGGTGAGAGGAAACAGAAAAA
 TCACAAATAGGCTAAGAAGTTGAACACTATATTTATCTTGTGAGTTTTATATTAAAGAAAGAAATACATTGT
 AAAAATGTCAAGAAAGTATGATCATCTAATGAAAGCCAGTTACACCTCAGAAAAATGATTTCCAAAAAATTA
 AAACCTACTAGTTTTTTTTCACTGTGGAGGATTCTCATTACTCTACAACTTGTATTATTTTTCTATTCAAT
 AAAAGCCCTAAACAACTAAATGATTGATTCTATACCCCACTGAATTCAAGCTGATTAAATTTAAATTT
 GGTATGCTGAAGTCTGCCAAGGTACATTATGGCCATTTTAAATTACAGCTAAATATTTTTTAAATGCA
 TTGCTGAGAACGTTGCTTTCATCAACAAAGATAAATATTTTTTCAGAAGTAA

0951161.11601

FIGURE 147

MKALLLLVLPWLSPANYIDNVGNLHFLYSELCKGASHYGLTKDRKRRSQDGC PDGCASLTAT
APSPPEVSAAATISLMTDEPGLDNPAYVSSAEDGQPAISPVDSGRSNRTRARPFERSTIRSRS
FKKINRALSVLRRTKSGSAVANHADQGRENSENTTAPEVFPRLYHLIPDGEITSIKINRVDP
SESLSIRLVGGSETPLVHII IQHIYRDGVIARDGRLLPGDIILKVNGMDISNVPHNYAVRLL
RQPCQVLWLTVMREQKFRSRNNGQAPDAYRPRDDSFHVILNKSSPEEQLGIKLVVRKVDEPGV
FIFNVLDGGVAYRHGQLEENDRVLAINGHDRLYGPSESAHLIQASERRVHLVVSQRQVRQS
PDIFQEAGWNSNGSWSPGPGERSNTPKPLHPTITCHEKVVNIQKDPGESLGMTVAGGASHRE
WDLPIYVISVEPPGGVISRDGRIKTGDILLNV DGVELTEVSRSEAVALLKRTSSSIVLKALEV
KEYEPQEDCSSPAALDSNHNMAPPSDWSPSWVMWLELPRCLYNCKDIVLRRNTAGSLGFCIV
GGYEEYNGNKPFPIKSIVEGTPAYNDGRIRC DILLAVNGRSTSGMIHACLARLLKELKGRI
TLTIVSWPGTFL

09551211601

FIGURE 148

CCAAAGTGATCATTTGAAAAAGAGATATCCACATCTTCAAGCCCATATAAAGGATAGAAGCT
GCACAGGGCAGCTTTACTTACTCCAGCACCTTCCTCTCCCAGGCAAATGGTGCTGACCATCT
TTGGGATACAATCTCATGGATACGAGGTTTTTAACATCATCAGCCCAAGCAACAATGGTGCC
AATGTTTCAGGAGACAGTGACAATTGATAATGAAAAAATACCGCCATCGTTAACATCCATGC
AGGATCATGCTCTTCTACCACAATTTTGGACTATAAACATGGCTACATTGCATCCAGGTGC
TCTCCCGAAGAGCCTGCTTTATCCTGAAGATGGACCATCAGAACATCCCTCCTCTGAACAAT
CTCCAATGGTACATCTATGAGAAACAGGCTCTGGACAACATGTTCTCCAACAAATACACCTG
GGTCAAGTACAACCCCTCTGGAGTCTCTGATCAAAGACGTGGATTGGTTCCTGCTTGGGTCAC
CCATTGAGAACTCTGCAAACATATCCCTTTGTATAAGGGGAAGTGGTTGAAAACACACAT
AATGTCGGTGCTGGAGGCTGTGCAAAGGCTGGGCTCCTGGGCATCTTGGGAATTTCAATCTG
TGCAGACATTCATGTTTAGGATGATTAGCCCTCTTGTTTTATCTTTTCAAAGAAATACATCC
TTGGTTTACACTCAAAGTCAAATTAATCTTTCCCAATGCCCCAACTAATTTTGAGATTC
AGTCAGAAAATATAAATGCTGTATTTATA

149/330

FIGURE 149

MKILVAFVLVLTIFGIQSHGYEVFNIISPSNNGGNVQETVTIDNEKNTAIVNIHAGSCSSTT
IFDYKHGYIASRVLSRRACFILKMDHQNIPLNQLQWYIYEKQALDNMFSNKYTWVKYNPLE
SLIKDVDWFLGSPIEKLCKHIPLYKGEVVENTHNVGAGGCAKAGLLGILGISICADIHV

0991181.11601

FIGURE 150

GGCACGAGCCAGGAAGTCTAGGAGGTTCTCACTGCCCCGAGCAGAGGCCCTACACCCACCGAGGC
ATGGGGCTCCCTGGGCTGTTCTGCTTGGCCGTGCTGGCTGCCAGCAGCTTCTCCAAGGCACG
 GGAGGAAGAAATTACCCCTGTGGTCTCCATTGCCTACAAAGTCTGGAAGTTTTCCCCAAAG
 GCGCTGGGTGCTCATAACTGCTGTGCACCCAGCCACCACCGCCATCACCTATTCCTTC
 TGTGGAACCAAGAACATCAAGGTGGCCAAGAAGGTGGTGAAGACCCACGAGCCGGCCTCCTT
 CAACCTCAACGTCACACTCAAGTCCAGTCCAGACCTGCTCACCTACTTCTGCCGGGCGTCCT
 CCACCTCAGGTGCCCATGTGGACAGTGCCAGGCTACAGATGCACTGGGAGCTGTGGTCCAAG
 CCAGTGTCTGAGCTGCGGGCCAACCTTCACTCTGCAGGACAGAGGGGCAGGCCCCAGGGTGGA
 GATGATCTGCCAGGCGTCTCGGGCAGCCACCTATCACCAACAGCCTGATCGGGAAGGATG
 GGCAGGTCCACCTGCAGCAGAGACCATGCCACAGGCAGCCTGCCAACTTCTCCTTCCTGCCG
 AGCCAGACATCGGACTGGTTCTGGTGCAGGCTGCAAAACACGCCAATGTCCAGCACAGCGC
 CCTCACAGTGGTGCCCCAGGTGGTGACCAGAAGATGAGGAGACTGGCAGGGTCCCCCTGGAGA
 GCCCCATCCTTGCTTGCCGCTCTACAGGAGCACCCGCCGTCTGAGTGAAGAGGAGTTTGGG
 GGGTTCAGGATAGGGAATGGGGAGGTCAGAGGACGCAAGCAGCAGCCATG**TAGA**AATGAACC
 GTCCAGAGAGCCAAGCACGGCAGAGGACTGCAGGCCATCAGCGTGCACTGTTCTGATTTGGA
 GTTCATGCAAAATGAGTGTGTTTTAGCTGCTCTTGCCACAAAAAAAAAAAAAAAAAAAAA

0991131 111601
 1011131 1211660

FIGURE 151

MGLPGLFCLAVLAASSFSKAREEEITPVVSIAYKVLEVFPKGRWVLITCCAPQPPPPITYSL
CGTKNIKVAKKVVKTHEPASFNLVTLKSSPDLLTYFCRASSTSGAHVDSARLQMHWELWSK
PVSELRANFTLQDRGAGPRVEMICQASSGSPITNSLIGKDQVHLQQRPCHRQPANFSFLP
SQTSDWFWCQAANNANVQHSALTVPVPPGGDQKMEDWQGPLESPILALPLYRSTRRLSEEEFG
GFRIGNGEVRGRKAAAM

Signal Peptide:

amino acids 1-18

N-glycosylation Sites:

amino acids 86-89, 132-135, 181-184

FIGURE 152

GGTCCTTA**ATG**GCAGCAGCCGCCGCTACCAAGATCCTTCTGTGCCTCCCGCTTCTGCTCCTG
 CTGTCCGGCTGGTCCCGGGCTGGGCGAGCCGACCCTCACTCTCTTTGCTATGACATCACCGT
 CATCCCTAAGTTCAGACCTGGACCACGGTGGTGTGCGGTTCAAGGCCAGGTGGATGAAAAGA
 CTTTTCTTCACTATGACTGTGGCAACAAGACAGTCACACCTGTCACTCCCTGGGGAAGAAA
 CTAAATGTCACAACGGCCTGGAAAGCACAGAACCCAGTACTGAGAGAGGTGGTGGACATACT
 TACAGAGCAACTGCGTGACATTAGCTGGAGAATTACACACCCAAAGGAACCCCTCACCTGCG
 AGGCAAGGATGTCTTGTGAGCAGAAAAGCTGAAGGACACAGCAGTGGATCTTGGCAGTTCAGT
 TTCGATGGGCAGATCTTCTCCTCTTTGACTCAGAGAAGAGAATGTGGACAACGGTTCATCC
 TGGAGCCAGAAAGATGAAAGAAAAGTGGGAGAATGACAAGGTTGTGGCCATGTCCTTCCATT
 ACTTCTCAATGGGAGACTGTATAGGATGGCTTGAGGACTTCTTGATGGGCATGGACAGCACC
 CTGGAGCCAAGTGCAGGAGCACCCTCGCCATGTCTCAGGCACAACCCAACTCAGGGCCAC
 AGCCACCACCCCTCATCCTTTGCTGCCTCCTCATCATCTCCCTGCTTTCATCTCCCTGGCA
 TCTGAGGAGAGTCCTTTAGAGTGACAGGTTAAAGCTGATACCAAAAGGCTCCTGTGAGCAG
 GTCTTGATCAAACTCGCCCTTCTGTCTGGCCAGCTGCCCACGACCTACGGTGTATGTCAGT
 GGCTCCAGCAGATCATGATGACATCATGGACCAATAGCTCATTCACTGCCTTGATTCCTT
 TTGCCAACAAATTTTACCAGCAGTTATACCTAACATATTATGCAATTTTCTCTTGGTGCTACC
 TGATGGAATTCCTGCACTTAAAGTTCTGGCTGACTAAACAAGATATATCATTTTCTTCTTC
 TCTTTTGTGTTGGAAAATCAAGTACTTCTTTGAATGATGATCTCTTCTTGCAAAATGATATT
 GTCAGTAAAATAATCAGTTAGACTTCAGACCTCTGGGGATTCTTTCCTGTGCTGAAAGAG
 AATTTTTAAATTATTTAATAAGAAAAAATTTATATTAATGATTGTTTCTTTAGTAATTTAT
 TGTCTGTACTGATATTTAAATAAAGAGTTCTATTTCCCAAAAAAAAAAAAAAAAAA

FIGURE 153

MAAAAATKILLCLPLLLLLSGWSRAGRADPHSLCYDITVIPKFRPGPRWCAVQGQVDEKTFI
HYDCGNKTVTPVSPGLGKLNVTTAWKAQNPVLREVVDILTEQLRDIQLENYTPKEPLTLQAR
MSCEQKAEGHSSGSWQFSFDGQIFLLFDSEKRMWTTVHPGARKMKEKWENDKVVAMSFHYFS
MGDCIGWLEDFLMGMDSTLEPSAGAPLAMSSGTTQLRATATTLLCCLLIILPCFILPGI

Important features:**Signal peptide:**

amino acids 1-25

Transmembrane domain:

amino acids 224-246

N-glycosylation site.

amino acids 68-72, 82-86

N-myristoylation site.

amino acids 200-206, 210-216

Amidation site.

amino acids 77-81

FIGURE 154

GGGAAAGCCATTTGAAAACCCATCTATACAACTATATATTTTCATTTCTGCTGCTAGCTG
CCTTGGGCCTCACAATTTTCATTCTGTTTCTGACTTTCAGTTATATACCGTGGAAATGGAG
TTGATCCCAACCATAACATCGTGGAGGGTTTTAATTTGGTGGTAGCCCTCACCCAATTCTG
GTGTGGCTTTCTTTGCAGAGGATTCCACCTTCAAAATCATGAACCTCTGGCTGTTGATCAAAA
GAGAATTTGGATTCTACTCTAAAAGTCAATATAGGACTTGGCAAAAGAAGCTAGCAGAAGAC
TCAACCTGGCCTCCCATAAACAGGACAGATTATTAGGTGATGGCAAAATGGATTCTACAT
CAACGGAGGCTATGAAAGCCATGAACAGATTCCAAAAAGAAAACCTCAAATTGGGAGGCCAAC
CCACAGAACAGCATTTCTGGGCCAGGCTGTAATCAGAATTGTCGTCGTACATGCTCAACAGC
ATTGCTTTTTTCCCCAAAATTAACACATTGTGGAGAAGTGATGATACTCTCCCTTACCTTT
CCTCTCTCCATTCAAGCATTCAAAGTATATTTTCAATGAATTAAACCTTGCAGCAAGGGACC
TTAGATAGGCTTATTCTGACTGTATGCTTTACCAATGAGAGAAAAAATGCATTTCTCTGTAT
CATCCTTTTCAATAAACTGTATTCAATTTGAAAAAAAAAAAAAAAAAAAAA

155/330

FIGURE 155

MELIPTITSWRVLILVVALTQFCGFLCRGFHLQNHFWLLIKREFGFGYSKSQYRTWQKKLA
EDSTWPPINRTDYSGDGKNGFYINGGYESHEQIPKRKLKLGQPTEQHFWARL

09TTT:18TT660

FIGURE 156

GTTCTCCTTTCCGAGCCAAAATCCCAGGCGATGGTGAATTATGAACGTGCCACACC**ATGAAG**
 CTCTTGTGGCAGGTAACGTGTGCCACCCACACCTTGGAAATGCCATCCTGCTCCCGTTTCGTCTA
 CCTCACGGCGCAAGTGTGGATTCTGTGTGCAGCCATCGCTGCTGCCGCCTCAGCCGGGCCCC
 AGAACTGCCCTCCGTTTGTCTGTGCAGTAACAGTTCAGCAAGTGGTGTGTGCACGGCCGG
 GGCTCTCCGAGGTCCCGCAGGGTATTCCCTCGAACACCCGGTACCTCAACCTCATGGAGAA
 CAACATCCAGATGATCCAGGCGGACACCTTCCGCCACCTCCACACCTGGAGGTCTCTGCAGT
 TGGGCAGGAACCTCCATCCGGCAGATTGAGGTGGGGGCCTTCAACGGCCTGGCCAGCCTCAAC
 ACCCTGGAGCTGTTGCAACAACCTGGCTGACAGTCATCCCTAGCGGGGCCTTTGAATACCTGTC
 CAAGCTCGGGGAGCTCTGGCTTCGCAACAACCCCATCGAAAGCATCCCTCTTACGCCTTCA
 ACCGGGTGCCCTCCCTCATGCGCCTGGACTTGGGGGAGCTCAAGAAGCTGGAGTATATCTCT
 GAGGGAGCTTTTGAAGGGGTGTTCACCTCAAGTATCTGAACTTGGGCATGTGCAACATTAA
 AGACATGCCCAATCTCACCCCCCTGGTGGGGCTGGAGGAGCTGGAGATGTGAGGGAACCACT
 TCCCTGAGATCAGGCCTGGCTCCTTCCATGGCCTGAGCTCCCTCAAGAAGCTCTGGGTCATG
 AACTCACAGGTGAGCTGATTGAGCGGAATGCTTTTGACGGGCTGGCTTCACTTGTGGAACCT
 CAACTTGGCCCAACAATAACCTCTCTTCTTTGCCCATGACCTCTTTACCCCGCTGAGGTACC
 TGGTGGATTGTGATCTACACCACAACCTTGGAACTGTGATTGTGACATTTCTGTGGCTAGCC
 TGGTGGCTTGCAGAGTATATACCCACCAATTCCACCTGCTGTGGCCGCTGTATGCTCCCAT
 GCACATGCGAGGCGGCTACCTCGTGGAGGTGGACAGGGCCTCCTTCCAGTGCTCTGCCCCCT
 TCATCATGGACGCACCTCGAGACCTCAACATTTCTGAGGGTGGATGGCAGAACTTAAAGTGT
 CGGACTCCCCCTATGTCTCCGTGAAGTGGTGTGCTGCCCAATGGGACAGTGCTCAGCCACGC
 CTCCCGCCACCCAAGGATCTCTGTCTCAACGACGGCACCTTGAACCTTTTCCACAGTGCTGC
 TTTGAGACACTGGGGGTACACATGCATGGTGACCAATGTTGAGGCAACTCCAACGCCTCG
 GCCTACCTCAATGTGAGCAGCGCTGAGCTTAACACCTCCAACCTACAGCTTCTTCAACCACAGT
 AACAGTGGAGACCAACGGAGATCTCGCCTGAGGACACACGCGGAAAGTACAAGCCTGTTCCCTA
 CCAGTCCACTGTTTACCAGCGGCATATACCACCTCTACCACGGTGCTCATTGAGACTACC
 CGTGTGCCCAAGCAGGTGGCAGTACCCGCGACAGACACCACTGACAAGATGCAGACAGCCCT
 GGATGAAGTCATGAAGACCACCAAGATCATCATTGGCTGCTTTGTGGCAGTGACTCTGCTAG
 CTGCCGCCATGTTGATTGTCTTCTATAAACTTCGTAAGCGGCACAGCAGCGGAGTACAGTC
 ACAGCGCCCGGACTGTTGAGATAATCCAGGTGGACGAGACATCCAGCAGCAACATCCGC
 AGCAGCAACAGCAGCTCCGTCCGGTGATCAGGTGAGGGGGCAGTAGTGCTGCCCACAATTC
 ATGACCATATTAACACACCTACAAACCAGCACATGGGGCCCACTGGACAGAAAACAGC
 CTGGGGAACCTCTCTGACCCACAGTCACCACTATCTCTGAACCTTATATAATTGAGACCA
 TACCAAGGACAGGTACAGGAACTCAAAT**TGACT**CCCCCCCCCAAACTTATAAAAT
 GCAATAGAAATGCACAAAGACAGCAACTTTGTACAGAGTGGGAGAGACTTTTCTTGTA
 TATGCTTATATTAAGTCTATGGGCTGGTAAAAAAAACAGATTATATTAAATTTAAAGA
 CAAAAGTCAAAACA

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FIGURE 159

MELGCWTQLGLTFLQLLLISSLPREYTVINEACPGAENWIMCRECCEYDQIECVCPGKREVV
GYTIPCCRNEENECDSCLIHPGCTIFENCKSCRNGSWGGLDDFYVKGFYCAECRAGWYGGD
CMRCGQVLRAPKGQILLESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRD
GDNRDQIIKRVCNERPAPIQSIGSSLHVLFHSDGSKNFDGPFHAIYEEITACSSSPCFHDG
TCVLDKAGSYKCACLAGYTGQRCENLLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGTV
VSFFCNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISDLVRRRVLPMQVQSRETPLH
QLYSAAFSKQKLSAPTKKPALPFGDLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGK
WSGRAPSCIPICGIENITAPKTQGLRWPWQAAIYRRTSGVHDGSLHKGAWFLVCSGALVNE
RTVVVAHCVTDLGKVTMIKTADLKVVLGKFYRDDDRDEKTIQSLQISAIILHPNYDPILLD
ADIAILKLLDKARISTRVQPICLAASRDLSFSQESHITVAGWNVLADVRSPGFKNDTLRSG
VVSVDLLCEEQHEDHGI PVSVTDNMFASWEPTAPSDICTAETGGIAAVSFPPGRASPEPR
WHLMGLVSWSYDKTCSHRLSTAFTKVLPPFKDWIERNMK

FIGURE 160

ACCAGGCATTGTATCTTCAGTTGTCATCAAGTTCGCAATCAGATTGGAAAAGCTCAACTTGA
 AGCTTTCCTTGCCCTGCAGTGAAGCAGAGAGATAGATATTATTACAGTAATAAAAAAC**ATG**GGC
 TTCAACCTGACTTCCACCTTTCCTACAAATTCCGATTACTGTTGCTGTTGACTTTGTGSCCT
 GACAGTGGTTGGGTGGGCCACCACTAACTACTTCGTGGGTGCCATTCAAGAGATTCCCTAAAG
 CAAAGGAGTTTATGGCTAATTTCCATAAGACCCCTCATTTTGGGGAAGGGAAAACTCTGACT
 AATGAAGCATCCACGAAGAAGGTAGAAGCTTGACAACTGTCCTTCTGTGTCTCCTTACCTCAG
 AGGCCAGAGCAAGCTCATTTTCAAACCAGATCTCAGTTTGGGAAGAGGTACAGGCAGAAAAATC
 CCAAAGTGTCCAGAGGCCGGTATCGCCCTCAGGAATGTAAGGCTTACAGAGGGTCGCCATC
 CTCGTTCCCCACCGAACAGAGAGAAAACCTGATGTACCTGCTGGAACATCTGCATCCCTT
 CCTGCAGAGGCAGCAGCTGGATTATGGCATCTACGTCATCCACCAGGCTGAAGGTAAGGATC
 TTAATCGAGCCAACTCTTGAATGTGGGCTATCTAGAAGCCCTCAAGGAAGAAAAATGGGAC
 TGCCTTATATTCCAGCATGTGGACCTGGTACCCGAGAACTGACTTTAACCTTTACAAGTGTGA
 GGAGCATCCCAAGCATCTGGTGGTTGGCAGGAACAGCACTGGGTACAGGTTACGTTACAGTG
 GATATTTTGGGGGTGTTACTGCCCTAAGCAGAGAGCAGTTTTCAGGTTGAATGGATTCTCT
 AACAACCTACTGGGGATGGGGAGGCGAAGACGATGACCTCAGACTCAGGGTTGAGCTCCAAAG
 AATGAAAATTTCCCGGCCCTGCCTGAAGTGGGTAAATATACAATGGTCTTCCACACTAGAG
 ACAAGGCAATGAGGTGAACGCAGAACGGATGAAGCTCTTACACCAAGTGTACAGAGTCTGG
 AGAACAGATGGGTGAGTAGTTGTTCTTATAAAATAGTATCTGTGGAACACAATCCTTTATA
 TATCAACATCAGAGTGGATTCTGGTTTGGTGCAT**GA**CCCTGGATCTTTTGGTGATGTTTGG
 AAGAAGCTGATTCTTTGTTTGCATAATTTTGGCCTAGAGACTTCAAATAGTAGCACACATTA
 AGAACCTGTTACAGCTCATTGTTGAGCTGAATTTTTCCTTTTGTATTTTCTTAGCAGAGCT
 CCTGGTGATGTAGAGTATAAAACAGTTGTAACAGACAGCTTCTTAGTCATTTTGATCATG
 AGGGTTAAATATGTAAATATGGATACTTGAAGGACTTTATATAAAAGGATGACTCAAAGGAT
 AAAATGAACGCTATTTGAGGACTCTGGTTGAAGGAGATTTATTTAAATTTGAAGTAATATAT
 TATGGGATAAAAGGCCACAGGAATAAGACTGCTGAATGTCTGAGAGAACCAGAGTTGTTCT
 CGTCCAAGGTAGAAAGGTACGAAGATACAATACTGTTATTATTTATCTGTACAATCATCT
 GTGAAGTGGTGGTGTGAGGTGAGAAGCGCTCCACAAAAGAGGGGAGAAAAGCGCAGCAATCA
 GGACACAGTGAAGTTGGGAATGAAGAGGTAGCAGGAGGGTGGAGTGTCTGGCTGCAAAGGCAG
 CAGTAGCTGAGCTGGTTGCAGGTGCTGATAGCCTTCAGGGGAGGACCTGCCAGGTATGCCT
 TCCAGTGATGCCACCAGAGAATACATTCTCTATTAGTTTATAAGAGTTTTGTAAAAATGA
 TTTTGTACAAGTAGGATATGAATTAGCAGTTTACAAGTTTACATATTAACTAATAATAATA
 TGTCTATCAAATACCTCTGTAGTAAATGTGAAAAAGCAAAA

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FIGURE 161

MGFNLTFHLSYKFRLLLLLTLCLTVVGWATSNYFVGAIQEIPKAKEFMANFHKTLLLGKGKT
LTNEASTKKVELDNCPSVSPYLRGQSKLIFKPDLTLEEVQAENPKVSRGRYRPQECKALQRV
AILVPHRNREKHLMYLLEHLHPFLQRQQLDYGIVYIHQAEGKKFNRAKLLNVGYLEALKEEN
WDCFIHFDVDLVPENDFNLYKCEEHPKHLVGRNSTGYRLRYSGYFGGVTALSREQFFKVNG
FSNNYWGWWGGEDDLRLRLVELQRMKISRPLPEVGKYTMVFHTRDKGNEVNAERMKLLHQVSR
VVRTDGLSSCSYKLVSVEHNPLYINITVDFWFGA

Important features:**Signal peptide:**

amino acids 1-27

N-glycosylation sites:

amino acids 4-7, 220-223 and 335-338

Xylose isomerase proteins:

amino acids 191-201

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1011.1811660

FIGURE 163

MAQAVWSRLGRILWLACLLPWAPAGVAAGLYELNLTDSPTTGA VVTISASLVAKDNGSLA
LPADAHLYRFHWIHTPLVLTGKMEKGLSSTIRVVGHVPGEFPVSVWVTAADCWMCQPVARGF
VVLPITEFLVGDLVVTQNTSLPWPSSYLTKTVLKVSFLLHDP SNFLKTALFLYSWDFGDGTQ
MVTEDSVVYYNYSIIGTFTVKLKVVAEWEEVEPDATRAVKQKTGDFSASLKLQETLRGIQVL
GPTLIQTQFKMTVTILNFLGSPPLTVCWRLKPECLPLEEGECHPVSVASTAYNLTHTRDPGD
YCF SIRAENIISKTHQYHKIQVWPSRIQPAVFAFP CATLITVMLAFIMYMTLRNATQQKDMV
ENPEPPSGVRCCQMC CGPFLLLETPSEYLEIVRENHGLLPPLYKSVKTYTV

Important features of the protein:**Signal peptide:**

amino acids 1-24

Transmembrane domain:

amino acids 339-362

N-glycosylation sites.

amino acids 34-37, 58-61, 142-145, 197-200, 300-303 and 364-367

FIGURE 164

GCTCAAGACCCAGCAGTGGGACAGCCAGACAGACGGCACG**ATG**GCACTGAGCTCCCAGATCT
GGGCCGCTTGCCTCCTGCTCCTCCTCCTCGCCAGCCTGACCACTGGCTCTGTTTTCCCA
CAACAGACGGGACAACCTTGCAAGCTGCAACCCAGGACAGAGCTGGAGCCAGGGCCAGCTG
GATGCCCCATGTTCCAGAGGCGAAGGAGGCGAGACACCCACTTCCCCATCTGCATTTTCTGCT
GCGGCTGCTGTCATCGATCAAAGTGTGGGATGTGCTGCAAGACG**TAG**AACCTACCTGCCCTG
CCCCGTCCCTCCCTTCCTTATTTATTCCTGCTGCCCCAGAACATAGGTCTTGGAATAAAA
TGGCTGGTTCTTTGTTTTCCAAA
AAA

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165/330

FIGURE 165

MALSSQIWAACLLLLLLASLTSGSVFPQQTGQLAELQPQDRAGARASWMPMFQRRRRRDTH
FPICIFCCGCCHRSKCGMCCKT

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FIGURE 166

CTGTCAGGAAGGACCATCTGAAGGCTGCAATTTGTTCTTAGGGAGGCAGGTGCTGGCCTGGC
 CTGGATCTTCCAC**CATG**TTTCCTGTTGCTGCTTTTGATAGCCTGATTGTCAACCTTCTGGGC
 ATCTCCCTGAGCTGTCTCTTCCACCTCCTTCTCGTTTTTCATCATAGTGCCAGCCATTTTGG
 AGTCTCCTTTGGTATCCGCAAACTCTACATGAAAAGTCTGTTAAAAATCTTTGCGTGGGCTA
 CCTTGAGAAATGGAGCGAGGAGCCAAAGGAGAAGAACCACCACTTTACAAGCCCTACACCAAC
 GGAATCATTTGCAAAAGGATCCCACTTCACTAGAAGAAGAGATCAAAGAGATTCGTCGAAGTGG
 TAGTAGTAAGGCTCTGGACAACACTCCAGAGTTTCGAGCTCTCTGACATTTTCTACTTTTGCC
 GGAAGGAATGGAGACCATTATGGATGATGAGGTGACAAAGAGATTCTCAGCAGAGAAGCTG
 GAGTCTCGGAACCTGCTGAGCAGAACCAATTATAACTTCCAGTACATCAGCCTTCGGCTCAC
 GGTCTCTGGGGGTTAGGAGTGCTGATTTCGGTACTGCTTTCTGCTGCCGCTCAGGATAGCAC
 TGGCTTTTACAGGGATTAGCCTTCTGGTGGTGGGCACAACGTGGTGGGATACTTGCCAAAT
 GGGAGGTTTAAGGAATTCATGAGTAAACATGTTCACTTAATGTGTTACCGGATCTGCGTGCG
 AGCGCTGACAGCCATCATCACCTACCATGACAGGGAAAACAGACCAAGAAATGGTGGCATCT
 GTGTGGCCAAATCATACCTCACCGATCGATGTGATCATCTTTGGCCAGCGATGGCTATTATGCC
 ATGGTGGGTCAAGTGACCGGGGACTCATGGGTGTGATTACAGAGCCATGGTGAAGGCTG
 CCCACACGTCTGGTTTGAGCGCTCGGAAGTGAAGGATCGCCACCTGGTGGCTAAGAGACTGA
 CTGAACATGTGCAAGATAAAAGCAAGCTGCCTATCCTCATCTTCCCAGAAGGAACCTGCATC
 AATAATACATCGGTGATGATGTTCAAAAAGGGAAGTTTGAATTTGGAGCCACATTTTACCC
 TGTGCTATCAAGTATGACCTCAATTTGGCGATGCCTTCTGGAACAGCAGCAAAATACGGGA
 TGGTGACGTACCTGCTGCGAATGATGACCAGCTGGGCCATTGTCTGCAGCGTGTGGTACCTG
 CCTCCCATGACTAGAGAGGCAGATGAAGATGCTGTCCAGTTTGCGAATAGGGTGAATCTGTC
 CATTGCCAGGCAGGGAGGACTTGTGGACCTGCTGTGGGATGGGGGCTGAAGAGGGAGAAGG
 TGAAGGACACGTTCAAGGAGGAGCAGCAGAAGCTGTACAGCAAGATGATCGTGGGGAACAC
 AAGGACAGGAGCCGCTCT**CGA**GCCTGCCTCCAGCTGGCTGGGGCCACCGTGCGGGGTGCCAA
 CGGCTCAGAGCTGGAGTTGCCGCCGCCGCCCACTGCTGTGCTCTTTCAGACTCCAGGG
 CTCGCCGGGCTGCTCTGGATCCCAGGACTCCGGCTTTGCGCGAGCCGACGCGGGATCCCTGT
 GCACCCGGCGCAGCCTACCTTTGGTGGTCTAAACGGATGCTGCTGGGTGTTGCGACCCAGGA
 CGAGATGCCCTTGTTCTTTTACAATAAGTCGTTGGAGGAATGCCATTAAGTGAACCTCCCA
 CCTTTGACCGCTGTGCGGGCTGAGTGGTGGGGAGATGTGGCCATGGTCTTGTGCTAGAGAT
 GGCGGTACAAGAGTCTGTTATGCAAGCCCGTGTGCCAGGGATGTGCTGGGGGCGGCCACCCG
 CTCTCCAGGAAGGCACAGCTGAGGCACTGTGGCTGCGCTCAGCATCCACATCGCCCCAGC
 CTGTGGAGCTCTGCAGACATGATAGGAAGGAACTGTGATCTGCAGGGGCTTTCAGCAAAATG
 AAGGTTAGATTTTATGCTGCTGCTGATGGGGTTACTAAAGGAGGGGAAGAGGCCAGTG
 GGCCGCTGACTGGGCCATGGGGAGAAGCTGTGTTCTGTAAGCTCAAGGCTAACCCTGAACCTCCC
 ATGTGATGCGCGCTTGTGTGAATGTGTGCTCGGTTTCCCCTATGTGAATATGAGTCGGGGG
 GAATGGTGGTATTCCTACCTCACAGGGCTGTTGTGGGGATTAAGTGTGCTCGGGGTGAGTGA
 AGGACACATCAGCTTCAGTGTTCAAGTACAGGCCCAAAACGGGGCACGGCAGGCTGAG
 CTCAGAGCTGCTGCACTGGGCTTTGGATTTGTTCTTGTGAGTAAATAAACTGGCTGGTGAA
 TGA

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FIGURE 167

MFLLLPFDSLIVNLLGISLTVLFTLLLVIIVPAIFGVSGIRKLYMKSLLKIFAWATLRME
RGAKEKNHQLYKPYTNGIIAKDPTSLEEEIKEIRRGSSSKALDNTPEFELSDIFYFCRKGME
TIMDDEVTKRFSAEELSWNLLSRNTYNFYISLRLTVLWGLGVLIRYCFLLPLRIALFTG
ISLLVVGTTVVGYLPNGRFKEFMSKHVHLMCYRICVRALTAIITYHDRENRPNGGICVANH
TSPIDVILASDGYAMVGQVHGGLMGVIQRAMVKACPHVWFERSEVKDRHLVAKRLTEHVQ
DKSKLPILIFPEGTCINNTSVMMFKKGSFEIGATVYPVAIKYDPQFGDAFWNSSKYGMVTYL
LRMMTSWAIVCSVWYLPMTREADEDAVQFANRVKSAIARQGGLVDLLWDGGLKREKVKDTF
KEEQQKLYSKMIVGNHKDRSRS

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SCCCCTCGAAACCAAGGACTCCAGCACCTCTGGTCCCGCCCTCACCCGGAGCCCTGGCCCTCA
CGTCTCCTCCAGGCGATGCGCTGGCGGCTTTGATGATCGCCCTCGGCAGCCTCGGCCTCCAC
ACCTGGCAGGCCAGGCTGTTCCACCACCTCTGCCCTGGGCCTGGCTCCAGACACCTTTGA
CGATACCTATGTGGGTTGTGCAGAGGAGATGGAGGAGAAGGCAGCCCCCTGCTAAAGGAGG
AAATGGCCACCATGCCCTGCTGCGGGAAATCTCTGGGAGGCAGCCAGGAGACCTGGGAGGAC
AAGCGTCGAGGGCTTACCTTGCCCCCTGGCTTCAAAGCCCAGAATGGAATAGCCATTATGGT
CTACACCAACTCATCGAACACCTTGTACTGGGAGTTGAATCAGGCCGTGCGGACGGGCGGAG
GCTCCCGGAGCTCTACATGAGGCACTTTCCTTCAAAGCCCTGCATTCTACCTGATCCGG
GCCCTGCAGCTGCTGCGAGGCAGTGGGGCTGCAGCAGGGGACCTGGGGAGGTGGTGTCCG
AGGTGTGGGCAGCCTTCGCTTTGAACCCAAAGAGGCTGGGGACTCTGTCCGCTTGGGCCAGT
TTGCCTCCAGCTCCCTGGATAAGGCAGTGGCCACAGATTTGGGGAGAAGAGCGGGGCTGT
GTGTCTGCGCCAGGGGTGCAGCTAGGCTCACAATCTGAGGGGCTCCTCTCTGCCCCCTG
GAAGACTCTGCTCTTGGCCCCTGAGAGTTCCAGCTCTCAGGGTTGGGCCCTGAAGTCCA
ACATCTGCCACTTAGGAGCCCTGGGAACGGGTGACCTTCATATGACGAAGGCACCTCCAG
CAGCCTTGAGAAAGGAACATGGTTCCGACCGCAACCCCTAGCAGCCTTCTCCCCAACCAAG
ATGTTGGCTGGGGAGGCACAGCAGGGCTGAGGGAACCTCTGCTATGTGATGGGACTTCTCT
GGGACAAGCAAGGAAAGTACTGAGGCAGCCACTTGATTGAACGCTGTTGCAATGTGGAGACA
TGGAGTTTTATTGAGGTAGCTACGTGATTAAATGGTATTGCAGTGTGGA

169/330

FIGURE 169

MALAALMIALGSLGLHTWQAQAVPTILPLGLAPDTFDDTYVGC AEEMEEKAAPLLKEEMAHH
ALLRESWEAAQETWEDKRRGLTLPFGFKAQNGIAIMVYTNSNTLYWELNQAVRTGGGSREL
YMRHFPFKALHFYLIRALQLLRGSGGCSRGPGEVVFRGVGSLRFEPKRLGDSVRLGQFASS
LDKAVAHRFGEKRRGCVSAPGVQLGSQSEGASSLPWKTLTLLAPGEFQLSGVGP

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FIGURE 170

GTGGCTTCATTTTCAGTGGCTGACTTCCAGAGAGCAAT**ATG**GCTGGTTCCTCCCAACATGCCTCA
 CCCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCCTCTGGACCCGTGAAAGAGCTG
 GTCGGTTCCGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTCCAAAGTAAAGCAAGTTGACTC
 TATTGCTCTGGACCTTCAACACAACCCCTCTTGTCACCATACAGCCAGAAGGGGGCACTATCA
 TAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCAGATGGAGGCTACTCCCTGAAG
 CTCAGCAAACCTGAAGAAGAATGACTCAGGGATCTACTATGTGGGGATATACAGCTCATCACT
 CCAGCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACGAGCACCTGTCAAAGCCTAAAG
 TCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTGACCAATCTGACATGCTGCATG
 GAACATGGGGAAGAGGATGTGATTTATACCTGGAAGGCCCTGGGGCAAGCAGCCAATGAGTC
 CCATAATGGGTCCATCCTCCCCATCTCCTGGAGATGGGGAGAAAGTGATATGACCTTCATCT
 GCGTTGCCAGGAACCTGTGAGCAGAACTTCTCAAGCCCCATCCTTGCCAGGAAGCTCTGT
 GAAGGTGCTGCTGATGACCCAGATTCTCCATGGTCCCTCTGTGTCTCCTGTTGGTGCCCT
 CCTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTTGGTTTCTGAAGAGAGAGAGACAAGAAG
 AGTACATTGAAGAGAAGAAGAGAGTGGACATTTGTGCGGAAACTCCTAACATATGCCCCCAT
 TCTGGAGAGAAACACAGAGTACGACACAATCCCTCACACTAATAGAACAATCCTAAAGGAAGA
 TCCAGCAAATACGGTTTACTCCACTGTGGAATACCGAAAAAGATGGAAAAATCCCACTCAC
 TGCTCAGGATGCCAGACACCAAGGCTATTTGCCTATGAGAATGTTATCT**TAG**ACAGCAGTG
 CACTCCCCTAAGTCTCTGCTCA

171/330

FIGURE 171

MAGSPTCLTLIYILWQLTGSAAAGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPLVT
IQPEGGTIIIVTQNRNRERVDFFDGGYSLKLSKLLKKNDSGIYYVGIYSSSLQQPSTQEYVLHV
YEHLSPKPKVTMGLQSNKNGTCVTNLTCCEHGEEDVIYTWKALGQAANESHNGSILPISWRW
GESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLCLLLVPLLLSLFVLGLFLW
FLKRERQEEYIEKKRVDCRETFNICPHSGENTYDTPHNTRTILKEDPANTVYSTVEIP
KKMENPHSLLTMPDTPRLFAYENVI

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FIGURE 172

CTGGTTCCCCAACATGCCTCACCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCC
 TCTGGACCCGTGAAAGAGCTGGTCGGTCCGTGGTGGGGCCGTGACTTTCCCCCTGAAGTC
 CAAAGTAAAGCAAGTTGACTCTATTGTCTGGACCTTCAACACAACCCCTCTTGTACCATAC
 AGCCAGAAGGGGCACTATCATAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCCA
 GATGGAGGCTACTCCCTGAAGCTCAGCAAACCTGAAGAAGAATGACTCAGGGATCTACTATGT
 GGGGATATACAGCTCATCACTCCAGCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACG
 AGCACCTGTCAAAGCCTAAAGTCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTG
 ACCAATCTGACATGCTGCATGGAACATGGGAAGAGGATGTGATTTATACCTGGAAGGCCCT
 GGGGCAAGCAGCCAATGAGTCCCATAAATGGGTCCATCTCCCATCTCCTGGAGATGGGGAG
 AAAGTGATATGACCTTCATCTGCGTTGCCAGGAACCCTGTGAGCAGAAACTTCTCAAGCCCC
 ATCCTTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGACCCAGATTCTCCATGGTCCTCCT
 GTGTCTCCTGTTGGTGCCCTCCTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTTGGTTTC
 TGAAGAGAGAGAGACAAGAAGAGTACATTGAAGAGAAGAAGAGAGTGGACATTTGTCGGGAA
 ACTCCTAACATATGCCCCCATTTCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAA
 TAGAACAAATCCTAAAGGAAGATCCAGCAAATACGGTTTACTCCACTGTGGAAATACCGAAAA
 AGATGAAAAATCCCCACTCACTGCTCACGATGCCAGACACCAAGGCTATTTGCCTATGAG
 AATGTTATCTAGACAGCAGTGCCTCCCTAAGTCTCTGCTCAAAAAAAAAAAAAAAAAAAAA

FIGURE 173

GAAAGACGTGGTCCTGACAGACAGACAATCCTATTCCTACCAAAATGAAGATGCTGCTGCT
 GCTGTGTTTGGGACTGACCCTAGTCTGTGTCCATGCAGAAGAAGCTAGTTCTACGGGAAGGA
 ACTTTAATGTAGAAAAGATTAAATGGGGAATGGCATACTATTATCCTGGCCTCTGACAAAAGA
 GAAAAGATAGAAGAACATGGCAACTTTAGACTTTTTCTGGAGCAAATCCATGTCTTGGAGAA
 TTCCTTAGTTCTTAAAGTCCATACTGTAAGAGATGAAGAGTGCTCCGAATTATCTATGGTTG
 CTGACAAAACAGAAAAGGCTGGTGAATATTCTGTGACGTATGATGGATTCAATACATTTACT
 ATACCTAAGACAGACTATGATAACTTTCTTATGGCTCACCTCATTAAACGAAAAGGATGGGGA
 AACCTTCCAGCTGATGGGGCTCTATGGCCGAGAACCAGATTTGAGTTCAGACATCAAGGAAA
 GGTTTGCAACTATGTGAGGAGCATGGAATCCTTAGAGAAAATATCATTGACCTATCCAAT
 GCCAATCGCTGCCTCCAGGCCCGAGAATGAAGAATGGCCTGAGCCTCCAGTGTGAGTGGAC
 ACTTCTCACCAGGACTCCACCATCATCCCTTCCTATCCATACAGCATCCCCAGTATAAATTC
 TGTGATCTGCATCCATCCTGTCTCACTGAGAAGTCCAATTCCAGTCTATCAACATGTTACC
 TAGGATACCTCATCAAGAATCAAAGACTTCTTTAAATTTCTCTTTGATACACCCCTTGACAAAT
 TTTTCATGAAATTATTCCTCTTCCTGTTCAATAAATGATTACCCTTGCACTTAA

FIGURE 175

GGCTCGAGCGTTTCTGAGCCAGGGGTGACC**ATG**ACCTGCTGCGAAGGATGGACATCCTGCAA
 TGGATTGAGCCTGCTGGTTCTACTGCTGTTAGGAGTAGTTCTCAATGCGATACCTCTAATTG
 TCAGCTTAGTTGAGGAAGACCAATTTCTCAAACCCCATCTCTTGCTTTGAGTGGTGGTTC
 CCAGGAATTATAGGAGCAGGTCTGATGGCCATTCCAGCAACAACAATGTCCTTGACAGCAAG
 AAAAAGAGCGTGCTGCAACAACAGAACTGGAATGTTTCTTTTCATCATTTTTCAGTGTGATCA
 CAGTCATTGGTGCTCTGTATTGCATGCTGATATCCATCCAGGCTCTCTTAAAAGGTCCTCTC
 ATGTGTAATTCTCCAAGCAACAGTAATGCCAATTGTGAATTTTCATTGAAAAACATCAGTGA
 CATTTCATCCAGAATCCTTCAACTTGCAGTGGTTTTCAATGACTCTTGTCACCTCCTACTG
 GTTTCATAAAACCCACAGTAACGACACCATGGCGAGTGGCTGGAGAGCATCTAGTTTCCAC
 TTCGATTCTGAAGAAAAACAACATAGGCTTATCCACTTCTCAGTATTTTATAGTCTATTGCT
 TGTGGAATTCTGGAGGTCTGTTTGGGCTCAGTCAGATAGTCATCGGTTTCCTTGCGTCTC
 TGTGTGGAGTCTCTAAGCGAAGAAGTCAAATTGTG**TAG**TTTAATGGGAATAAAATGTAAGTA
 TCAGTAGTTTGAIAAAAAAAAA

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176/330

FIGURE 176

MTCCEGWTS CNGFSLLV LLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGLMA
IPATTM SLTARKRACCNRTGMFLSSFFSVITVIGALY CMLISIQALLKGPLMCNPSNSNA
NCEFS LKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGWRASSFHFDSEENKHRL
IHFSVFLG LLLVGILEVLFGLSQIVIGFLGCLCGVSKRRSQIV

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FIGURE 177

GTCGAATCCAAATCACTCATTGTGAAAGCTGAGCTCACAGCCGAATAAGCCACCATGAGGCT
GTCAGTGTGTCTCCTGATGGTCTCGCTGGCCCTTTGCTGCTACCAGGCCCATGCTCTTGTCT
GCCCAGCTGTTGCTTCTGAGATCACAGTCTTCTTATTCTTAAGTGACGCTGCGGTAAACCTC
CAAGTTGCCAAACTTAATCCACCTCCAGAAGCTCTTGCAAGCCAAGTTGGAAGTGAAGCACTG
CACCGATCAGATATCTTTTAAGAAACGACTCTCATTGAAAAAGTCCTGGTGGAAATAGTGAA
AAAATGTGGTGTGTGACATGTAAAAATGCTCAACCTGGTTTCCAAAGTCTTTCAACGACACC
CTGATCTTCACTAAAAATGTAAAGGTTTCAACACGTTGCTTTAATAAATCACTTGCCCTGC

0991181-11601

178/330

FIGURE 178

MRLSVCLLMVSLALCCYQAHALVCPAVASEITVFLFLSDAAVNLQVAKLNPPPEALAAKLEV
KHCTDQISFKRRLSLKKSWWK

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FIGURE 179

ATCCGTTCTCTGCGCTGCCAGCTCAGGTGAGCCCTCGCCAAGGTGACCTCGCAGGACACTGG
TGAAGGAGCAGTGAGGAACCTGCAGAGTCACACAGTTGCTGACCAATTGAGCTGTGAGCCTG
GAGCAGATCCGTGGGCTGCAGACCCCGCCCCAGTGCCTCTCCCCCTGCAGCCCTGCCCTC
GAACTGTGACATGGAGAGAGTGACCCTGGCCCTTCTCCTACTGGCAGGCCTGACTGCCTTGG
AAGCCAATGACCATTGTGCCAATAAAGACGATCCCTTCTACTATGACTGGAAAAACCTGCAG
CTGAGCGGACTGATCTGCGGAGGGCTCCTGGCCATTGCTGGGATCGCGGCAGTTCTGAGTGG
CAAATGCAAATACAAGAGCAGCCAGAAGCAGCACAGTCCTGTACCTGAGAAGGCCATCCCAC
TCATCACTCCAGGCTCTGCCACTACTTGCTGAAGCACAGGACTGGCCTCCAGGGATGGCCTGA
AGCCTAACACTGGCCCCAGCACCTCCTCCCCTGGGAGGCCTTATCCTCAAGGAAGGACTTC
TCTCCAAGGGCAGGCTGTAGGCCCTTTCTGATCAGGAGGCTTCTTTATGAATTAACTCG
CCCCACCACCCCTCA

180/330

FIGURE 180

MERVTLALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGKCK
YKSSQKQHSVPVEKAIP LITPGSATTC

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FIGURE 182

MSLLSLPWLGIRPVAMSPWLLLLLVGSWLLARILAWTYAFYNNCRRLQCFQPQPKRNWFWG
HLGLITPTEEGLKDSTQMSATYSQGFTVWLGPIIPFIVLCHPDTIRSITNASAAIAPKDNLF
IRFLKPWLGEIGILLSGGDKWSRHRRLTPAFHFNILKSYITIFNKSANIMLDKWQHLASEGS
SRLDMEFHHISLMTLDSLQKCIFSFDSHCQERPSEYIATILELSALVEKRSQHILQHMDFLYY
LSHDGRRFHRACRLVHDFTDVIRERRRTLPTQGIDDFKDKAKSKTLDFIDVLLSKDEDEG
KALSDEDIRAEADTFMFGGHDTTASGLSWVLYNLARHPEYQERCQEVQELLKDRDPKEIEW
DDLAQLPFLTMCVKESLRLHPPAFFISRCCTQDIVLPDGRVIPKGITCLIDIIGVHHNPTVW
PDPEVYDPFRDPENSKGRSPLAFIPFSAGPRNCIGQAFAMAEMKVVLALMLLHFRFLPDHT
EPRRKLELIMRAEGLWLRVEPLNVGLQ

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FIGURE 183

CAACAGAAGCCAAGAAGGAAGCCGCTCTATCTTGTGGCGATCATGTATAAGCTGGCCTCCTGC
TGT TTGCTTTTACAGGATTCTTAATCCTCTCTATCTCTCCTCTCCTTGACTCCAGGGA
AATATCCTTTCAACTCTCAGCACCTCATGAAGACGCGCGCTTAATCCGGAGGAGCTAGAAA
GAGCTTCCCTTCTACAGATATTGCCAGAGATGCTGGGTGCAGAAAAGAGGGGATATTCTCAGG
AAAGCAGACTCAAGTACCAACATTTTAAACCAAGAGGAAATTTGAGAAAGTTTCAGGATTT
CTCTGGACAAGATCCTAACATTTTACTGAGTCATCTTTTGGCCAGAATCTGGAACCATACA
AGAAACGTGAGACTCCTGATTGCTTCTGGAAATACTGTGCTTGAAGTGAAATAAGCATCTGT
TAGTCAGCTCAGAAACACCCATCTTAGAATATGAAAATAACACAATGCTTGATTTGAAAC
AGTGTGGAGAAAACTAGGCCAACTACACCCTGTTTATTGTTACCTGGAAAATAAATCCTCT
ATGTTTTGCACAAAAAAAAAAAAAA

184/330

FIGURE 184

MYKLASCCLLFTGFLNPLLSLPLDSREISFQLSAPHEDARLTPEELERASLLQILPEMLGA
ERGDILRKADSSTNIFNPRGNLRKFQDFSGQDPNILLSHLLARIWKPYKKRETPDCFWKYCV

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186/330

FIGURE 186

MPSPGTVCSLLLGLWLDLAMAGSSFLSPEHQRVQQRKESKKPPAKLQPRALAGWLRPEDG
GQAEGAEDELEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADKO

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T09111.1811601

188/330

FIGURE 188

MNTWLLFLPLFPVQVQTLIVVVIIGMLVLLLDLGLVHLGQLLI FHIYLSMSPTLSPRSPQGW
VVRAAHLTPLLEYVPNPEPPTPGARVFVPRVRMCSGSASPRSEIMDKKGKSQEEIKSMRTQQ
AQQEAEELTPRPAGVVPGA

099181.11801

FIGURE 189

GGAGTGCAGATGGCATCCTTCGGTTCTTCCAGACAAGCTGCAAGACGCTGACCATGGCCAAG
 ATGGAGCTCTCGAAGGCCTTCTCTGGCCAGCGGACACTCCTATCTGCCATCCTCAGCATGCT
 ATCACTCAGCTTCTCCACAACATCCCTGCTCAGCAACTACTGGTTTGTGGGCACACAGAAGG
 TGCCCAAGCCCTGTGCGAGAAAGGTCTGGCAGCCAAGTGCTTTGACATGCCAGTGTCCCTG
 GATGGAGATACCAACACATCCACCCAGGAGGTGGTACAATACAACTGGGAGACTGGGGATGA
 CCGGTTCTCCTTCGGAGCTTCCGGAGTGGCATGTGGCTATCCTGTGAGGAACTGTGGAAG
 AACCAGGGGAGAGGTGCCGAAGTTTCATTGAACCTACACCACCAGCCAAGAGAGGTGAGAAA
 GGACTACTGGAATTTGCCACGTTGCAAGGCCATGTCACCCCACTCTCCGATTTGGAGGGAA
 GCGGTTGATGGAGAAGGCTTCCCTCCCTCCCTCCCTTGGGGCTTTGTGGCAAAAATCCTA
 TGGTTATCCCTGGGAACGCAGATCACCTACATCGGACTTCAATTCATCAGCTTCTCCTGCT
 ACTAACAGACTTGCTACTACTGGGAACCTGCCTGTGGGCTCAAAGTGAGCGCCTTTGCTG
 CTGTTTCTCTGTCTGTGAGGTCTCCTGGGGATGGTGGCCACATGATGTATTACAAAGTC
 TTCCAAGCGACTGTCAACTTGGGTCCAGAAGACTGGAGACCACATGTTTGAATTATGGCTG
 GGCTTCTACATGGCTGGCTCTCCTTCACCTGCTGCATGGCGTCGGCTGTCACCACTTCA
 ACACGTACACCAGGATGGTGCTGGAGTTCAGTGCAAGCATAGTAAGAGCTTCAAGGAAAAC
 CCGAACTGCCTACCACATCACCATCAGTGTTTCCCTCGGCGGCTGTCAAGTGCAGCCCCAC
 CGTGGGTCTTTGACCAGTACCACCAGTATCATAATCAGCCATCCACTCTGTCTCTGAGG
 GAGTCGACTTCTACTCCGAGCTGCGGAACAAGGGATTTCAAAGAGGGGCCAGCCAGGAGCTG
 AAGAAGCAGTTAGGTCATCTGTAGAGGAAGAGCAGTGTTAGGAGTTAAGCGGGTTTGGGGA
 GTAGGCTTGAGCCCTACCTTACACGCTGCTGATTATCAACATGTGCTTAAGCCAACATCCG
 TCTCTTGAGCATGGTTTTTAGAGGCTACGAATAAGGCTATGAATAAGGGTTATCTTTAAGTC
 CTAAGGGAATTCCTGGGTGCCACTGCTCTCTTTTCTCTACAGCTCCATCTGTTTACCCAC
 CCCACATCTCACACATCCAGAATTCCCTTCTTTACTGATAGTTTCTGTGCCAGGTCTTGGG
 TAAACCATGGAGATAAAAAGAAGAGTAAATACACTCCCCGACCTTAAGGATCTGAAA

190/330

FIGURE 190

MAKMELSKAFSGQRTLLSAILSMLSLSFSTTSLLSNYWFVGTQKVPKPLCEKGLAAKCFDMP
VSLDGDNTNTSTQEVVQYNWETGDDRF5FR5FRSGMWLSCEETVEEPGERCRSFIELTPPAKR
GEKGLLEFATLQGGPCHPTLRFGGKRLMEKASLSPPLGLCGKNPMVIPGNADHLHRTSIHQ
PPATNRLATHWEPCLWAQTERLCCCFLCPVRSPGDGGPHDVFTSLP5DCQLGSRRL5TT5CLE
LWLGLLHGLALLHLLHGVGCHHLQH5VHQDGAGVQVQA

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FIGURE 191

AACTGGAAGGAAAGAAAGAAAGGTGACGCTTTGGCCCA**ATG**TGGTTACCCCTTGGTCTCCTG
 TCTTTATGTCTTTCTCCTCTTCTATTTCTGTCACTCTCCCTCACTTAAGTCTCAGGCCGTGCA
 GCAGCTCCTGTGGACATTGCCATCCCCCTCTGGTAGCCTTCAGAGCAAACAGGACAACCTATG
 TTATGGATGTTTCCACCAACCAGGGTAGTGGCATGGAGCACCGTAACCATCTGTGCTTCTGT
 GATCTCTATGACAGAGCCACTTCTCCACCTCTGAAATGTTCCCTGCTCTGAAATCTGGCATG
 AGATGGCACAGGTGACCACGCAGAAGCCACCAGAATCTTGCCTGCCCTATTCTCCTCCCAA
 GTCTGTTCTCTTATTGTCAACCTCAGCACAAACAGGCTGGCGCCAATGGCATTACAGAGAAAG
 CAATCTGTGTGGCTAGTGGGCAGATTACCATGCAAGCCCCAGGAGAAATGGAGGAGCTTTGT
 AGCCACCTCCCTGTCAGCCAGTATTAACATGTCCCCCTCCCCCTGCCCGCCGTAGATTGAG
 GACATTCGCCCCCTGTGTGCCACCAACCAGGACTTCCCCCTTGGCTTGGCATCCCTGGCTCT
 CTCCTGGTACCCAGCAAGACGTCTGTTCCAGGGCAGTGTAGCATCTTCAAGCTCCGTACT
 ATGGCGATGGCCATGATGTACAATCCCACTTGCTGAATAATCAAGTGGGAAGGGGAAGCA
 GAGGAAATGGGCCATGTGAATGCAGCTGCTCTGTTCTCCCTACCGTGAGGAAAAACCAA
 GGGGAAGCAACAGGAACCTTCTGCAACTGGTTTTTATCGGAAAGATCATCCTGCCTGCAGATGC
 TGTGGAAGGGGCACAAGAAATGTAGCTGGAGAAGATTGATGAAAGTGCAGGTGTGTAAGGAA
 ATAGAACAGTCTGCTGGGAGTCAGACCTGGAATTCTGATCCAACTCTTTATTACTTTGGG
 AAGTCACTCAGCCTCCCCGTAGCCATCTCCAGGGTGACGGAACCCAGTGTTATTACCTGTGG
 AACCAAGGAAACTAACAATGTAGGTTACTAGTGAATACCCCAATGGTTTCTCCAATTATGCC
 CATGCCACCAAAACAATAAAACAAAATTCTCTAACACTGAAA

192/330

FIGURE 192

MWLPLGLLSLCLSPILSSPSLKSQACQQLLWTLPSPLVAFRANRTTYVMDVSTNQSGME
HRNHLCFCDLYDRATSPPLKCSLL

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194/330

FIGURE 194

MAGIKALISLSFGGAIGLMFLMLGICALPIYNKYWPLFVLFFYILSPIPYCIARRLVDDTDAM
SNACKELAIFLTGTGIVVSAFGLPIVFARAHLEWGACALVLTGNTVIFATILGFFLVFGSND
DFSWQQW

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[illegible]

FIGURE 196

MDFLLLGLCLYWLLRRPSGVVLCLLGACFQMLPAAPSGCFQLCRCEGRLLYCEALNLTEAPH
NLSGLLGLSLRYNSLSELRAGQFTGLMQLTWLYLDHNNHICSVQGDAFQKLRVKELTLSNQ
ITQLPNTTFRPMPNLRSDLSYNKLQALAPDLFHGLRKLTLHMRANAIQFVPVRIQDCRS
LKFLDIGYNQLKSLARNSFAGLFKLTLEHLEHNDLVKVNFAHFRLISLHSLCLRRNKVAIV
VSSLDWVWNLEKMDLSGNEIEYMEPHVFETVPHLQSLQLDSNRLTYIEPRILNSWKSLSIT
LAGNLWDCGRNVICALASWLSNFQGRYDGNLQCASPEYAQGEDVLDVYAFHLCEDGAEPTSG
HLLSAVTNRSDLGPPASSATTLADGGEGQHDGTFEPATVALPGGEHAENAVQIHKVVTGTMA
LIFSFLIVVLVLYVSWKCFPASLRQLRQCFVTQRRKQKQKQTMHQAAMSAQEYYVDYKPNH
IEGALV IINEYGSCTCHQQPARECEV

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FIGURE 197

GTGCAAGGAGCCGAGGCGAGATGGGCGTCCTGGGCCGGGTCTGCTGTGGCTGCAGCTCTGC
GCACTGACCCAGGCGGTCTCCAAACTCTGGGTCCCCAACACGGACTTCGACGTCGCAGCCAA
CTGGAGCCAGAACC GGACCCCGTGCGCCGGCGGC GCCGTTGAGTTCCCGCGGACAAGATGG
TGTCAGTCCTGGTGCAAGAAGGT CACGCCGTCTCAGACATGCTCCTGCCGCTGGATGGGGAA
CTCGTCCTGGCTTCAGGAGCCGGATTCCGGCGTCTCAGACGTGGGCTCGCACCTGGACTGTGG
CGCGGGCGAACCTGCCGTCTTCCGCGACTCTGACCGCTTCTCCTGGCATGACCCGCACCTGT
GGCGCTCTGGGGACGAGGCACCTGGCCTCTTCTTCGTGGACGCCGAGCGCGTGCCCTGCCGC
CACGACGACGTCTTCTTTCCGCCTAGTGCCTCCTTCCGCGTGGGGCTCGGCCCTGGCGCTAG
CCCCGTGCGTGTCCGCAGCATCTCGGCTCTGGGCCGGACGTTACGCGCGACGAGGACCTGG
CTGTTTTCTGGCGTCCCGCGCGGGCCGCTACGCTTCCACGGGCCGGCGCGCTTGAGCGTG
GGCCCCGAGGACTGCGCGGACCCGTCGGGCTGCGTCTGCGGCAACGCGAGGCGCAGCCGTG
GATCTGCGCGGCCCTGCTCCAGCCCCT

FIGURE 198

MGVLGRVLLWLQLCALTQAVSKLWVPNTDFDVAANWSQNRTPCAGGAVEFPADKMVSVLVQE
GHAVSDMLLPLDGELVLASGAGFGVSDVGSHLDCGAGEPAVFRDSDRFSWHDPLWRSDEA
PGLFFVDAERVPCRHDDVFFPPSASFRVGLGPGASPVVRVSISALGRFTFTRDEDLAVFLASR
AGRRLRFHGP GALSVGPEDCADPSGCVCGNAEAQPWICAALLQP

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[illegible]

200/330

FIGURE 200

MGPVKQLKRMFEPTRLIATIMVLLCFALTLCSAFWWHNKGLALIFCILQSLALTWYSLSFIP
FARDAVKKCFVCLA

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FIGURE 201

TTGAGCGCAGGTGAGCTCTCTGGCGGTTCCGGGGGCGTTCCCTCCAGTCAACCTCCCGCGGTACC CGCGGCGCGC
 CCAGAGGGAGTCTCTCCAGACCCCTCCCTCCCGTTGCTCCAAACTAATACGGACTGAACGGATTGCTGCGAGGGT
 GGGAGAGAAAATTAGGGGAGAAAAGGACAGAGAGAGCACTACCATCCATAGCCAGATAGATTATCTTACACTG
 AACTGATCAAGTACTTTGAAAGATGCTT CGAAATTTATCTTGGTGTCCCTCATCTGTGCTGCACTGAGTCTTTC
 AACCCAACTTTTCTCTCCAACTAGACCAGCAGAAAGGTTCTACTAGTTTCTTTTGTGATTGATTCCGTTGGGATTACT
 TATATAAAGTTTCCAAAGCCCCATTTTCATTATATTTGAAATATGGTGTTCACGTGAAGCAAGTTACTGAATGTT
 TTTTATACAAAACCTACCCCTAACCATTTATCTTTGGTAACCTGGCTCTTTGACAGAGAACTCATGGGATTGTTGC
 AAATGATATGTTTGATCCTATTCCGGAACAAATCTTCTCCTTGGATCACATGAATATTTATGATTCCAAGTTT
 GGGGAAGAGCGACCAATATGGATCACAAACAGAGGGCAGGACATCTAGTGGTGCAGCCATGTGCCCGGA
 ACAGATGTAAAAATACATAAGCGCTTCTCTACTCATTACATGCCTTACAATGAGTCAGTTTCATTTGAAGATAG
 AGTTGCCAAAATTTGTTGAATGTTTACGTCAAAGAGGCCATAAATCTTGGTCTTCTCTATTGGGAAGACCTTG
 ATGACATGGGCCACCATTTGGGACCTGACAGTCCGCTCATGGGGCTGTCAATTCAGATATTGACAAGAAGTTA
 GGATATCTCATACAAATGCTGAAAAGGCAAAGTTGTGGAACACTCTGAACCTAATCATCACAAAGTGATCATGG
 AATGACGCAGTGCTCTGAGGAAAAGTTAATAGAACTTGACCACTGACCTGGATAAAGACCACTATACCTGATTG
 ATCAATCTCCAGTAGCAGCCATCTTGCCAAAAGAAAGGTAATTTGATGAAGTCTATGAAGCACTAATCAGCT
 CATCCTAATCTTACTGTTTACAAAAGAAAGACGTTCCAGAAAGGTGGCATTACAAATACAACAGTCGAATTC
 ACCAATCATAGCAGTGGCTGATGAAGGTTGGCAGATTTTACAGAAATAGTCAGATGACTTCTGTTAGGCAACC
 ACGGTTACGATAATGCGTTAGCAGATATGCATCCAATATTTTACGCCATGGTCTGCTTCCAGAAAGAAATTC
 TCAAAGAAAGCCATGAACCTCCACAGATTTGTACCCACTACTATGCCACCTCTCAATATCACTGCCATGCCACA
 CAATGGATCATTTGGAATGTCAGGATCTGCTCAATTACGAATGCCAAGGGTGGTCCCTTATACACAGAGTA
 CTATACTCCTCCCTGGTAGTGTTAAACCAGCAGAAATGACCAAGAGGGGTATACCCCTTATTTATAGGGGTC
 TCTCTTGGCAGCATTTGATTGATTGATTTTGTATTTTTCATTAGCATTAAATCACAGTCAAATAGCTGC
 CTTACAAGATATGCATGCTGAAATAGTCAACCATATTACAGCCCTAATGTTACTTTGAAGTGGATTGCTATA
 TTGAAGTGGAGATTCATAAATTTATGCTAGTGTAAAGGTTTCAAATCTGGGAAACAGTTCCAAACATCTGC
 AGAACCATTAAAGCAGTTACATATTTAGGTATACACACACACACACACACACACACACACACAGGACAAA
 ATACTTACACCTGCAAAGGAATAAAGATGTGAGAGTATGTCTCCATTGTTCACTGTAGCATGGGATAGATAAG
 ATCCTGCITTAATTTGGACTTGGCGAGATAATGATATATTTAGCAACITTGACATATGTAAGTACCTTATAT
 ATTGCACITTTAAATTTCTCTCCTGATGGGTACTTAAATTTGAAATGCACTTTATGGACAGTTATGCTTTATAAC
 TTGATTGAAATGACACATTTTTCACCCATGTACAGAAATACITTTAGCATTGTTCAAACCTGAAGGAAATTT
 TCTAATAATCCGAAATAATGAACATAGAAATCTATCTCCATAAATTGAGAGAAGAAAGGGTGATAAGTGTGA
 AAATTAATGTGATAACCTTTGAACCTTGAATTTTGGAGATGATTCCCAACAGCAGAAATGCAACTGTGGGCAT
 TTCTTGTCTTATTTCTTCCAGAGAAGCTGGTTTCATTTATTTTCCCTCAAAGAGAGTCAAAATAGTGTGACAG
 ATTGGTTTCAAATATATTTCTTCTGTCATAAAATATTTGTGATTTCTGATGAGTCATATCTGTGATTTCA
 TAATAATGAGACACCATGAATATCTTTCTTCTATATAGTTACGAAATGGCCTGAATAGAAGCAACAGGCA
 CCATCTCAGCAATGTTTCTCTGTTGTAAATTTTGTCTCTTTGAAATTAATCACTATTAATTACATTAA
 AATCAATTTGGATAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGG

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FIGURE 202

MTSKFILVSFILAALSLSTTFSLQLDQQKVLVSVFDGFRWDYLYKVPTPHFHYIMKYGVHVK
 QVTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPIRKNKSFSLDHMNIYDSKFWEEATPIW
 ITNQIRAGHTSGAAMWPGTDVKIHKRFPTHYMPYNESVSFEDRVAKIVEWFTSKEPINLGLLY
 WEDPDDMGHHLLGPDSPIMGPVISDIDKKLGYLIQMLKKAKLWNTLNLIITSDHGMTQCSEER
 LIELDQYLDKDHYTELIDQSPVAAILPKEGKFDEVYEALTHAHPNLTVYKKEDVPERWHYKYN
 SRIQPIIAVADEGWHILQNKSDDFLLGNHGYDNALADMHPIFLAHGPAFRKNFSKEAMNSTD
 LYPLLCHLLNITAMPNGSFWNVQDLNLSAMPRVVPYQTSTILLPGSVKPAEYDQEGSYPIYF
 IGVSLGSIIVIVFFVIFIKHLIHSQIPALQDMHAEIAQPLLQA

Signal Peptide:

amino acids 1-22

Transmembrane Domain:

amino acids 429-452

N-glycosylation sites:

amino acids 101-104, 158-161, 292-295, 329-332, 362-365, 369-372, 382-385, 389-392

Somatomedin B Domain:

amino acids 69-85

Sulfatase protein Region:

amino acids 212-241

FIGURE 203

GGATTTTTGTGATCCGCGATTTCGCTCCACGGGCGGGACCTTTGTAAC TGCGGGAGGCCAG
 GACAGGCCACCCCTGCGGGGCGGAGGCAGCCGGGTGAGGGAGGTGAAGAAACCAAGACGC
 AGAGAGGCCAAGCCCCCTTGCCCTGCGGTACACAGCCAAAGGAGGCAGAGCCAGAATCACA
 CCAGATCCAGAGGCAACAGGGACATGGCCACCTGGGACGAAAAGGCAGTCACCCGAGGGCC
 AAGGTGGCTCCCCGCTGAGAGGATGAGCAAGTTCTTAAGGCACTTCACGGTCGTGGGAGACGA
 CTACCATGCCTGGAACATCAACTACAAGAAATGGGAGAATGAAGAGGAGGAGGAGGAGG
 AGCAGCCACCACCACACCAGTCTCAGGCGAGGAAGGCAGAGCTGCAGCCCCTGACGTTGCC
 CCTGCCCCCTGGCCCCGCACCCAGGGCCCCCCTTGACTTCAGGGGCATGTTGAGGAACTGTT
 CAGCTCCACAGGTTTCAGGTCATCATCATCTGCTTGGTGGTTCCTGGATGCCCTCCTGGTGC
 TTGCTGAGCTCATCCTGGACCTGAAGATCATCCAGCCCGACAAGAATAACTATGCTGCCATG
 GTATTCCACTACATGAGCATCACCATCTTGGTCTTTTTTATGATGGAGATCATCTTTAAATT
 ATTTGTCTTCCGCCTGAGTTCTTTACCACAAGTTTGAGATCCTGGATGCCCTCGTGGTGG
 TGGTCTCATTCATCCTGGACATTGTCTCCTGTTCCAGGAGCACCAGTTTGAGGCTCTGGGC
 CTGCTGATTCTGCTCCGGCTGTGGCGGGTGGCCCCGGATCATCAATGGGATTATCATCTCAGT
 TAAGACACGTTCAGAACGGCAACTCTTAAGGTTAAAACAGATGAATGTACAATTGGCCGCCA
 AGATTCAACACCTTGAGTTCAGCTGCTCTGAGAAGCCCCCTGGACTGATGAGTTTGCTGTATC
 AACCTGTAAGGAGAAGCTCTCTCCGGATGGCTATGGGAATGAAAGAAATCCGACTTCTACTCT
 CACACAGCCACCGTGAAAGTCCTGGAGTAAAATGTGCTGTGTACAGAAGAGAGAGAAGGAAG
 CAGGCTGGCATGTTCACTGGGCTGGTGTACGACAGAGAACCTGACAGTCACTGGCCAGTTA
 TCACTTCAGATTACAAATCACACAGAGCATCTGCCTGTTTTCAATCACAGAGAACAAAACC
 AAAATCTATAAAGATATTCTGAAAAATATGACAGAATTGACAAATAAAGCATAAACGTGTA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 204

MATWDEKAVTRRAKVAPAERMSKFLRHFTVVGGDYHAWNINYYKKWENEEEEEEEEQPPPTPV
SGEEGRAAAPDVAPAPGPAPRAPLDFRGMLRKLFSSHRFQVIIICLVVLDALLVLAELILD
KIIQPDKNNYAAMVFHYMSITILVFFMMEIIFKLFVFRLLSSFTTSLRSWMPVVVVVSFILD
VLLFQEHQFEALGLLILLRLWRVARIINGIIISVKTRSERQLLRKQMNVLAAKIQHLEFS
CSEKPLD

FIGURE 205

CGGCTCGAGCTCGAGCCGAATCGGCTCGAGGGGCGAGTGGAGCACCCAGCAGGCGGCCAACAT
 GCTCTGTCTGTGGCTGTACGTGCCGGTTCATCGGGGAAGCCAGACCGAGTTCCAGTACTTTG
 AGTCGAAGGGGCTCCCTGCCGAGCTGAAGTCCATTTTCAAGCTCAGTGTCTTCATCCCTCC
 CAGGAATTTCCACCTACCGCCAGTGGGAAGCAGAAAATTGTACAAGCTGGAGATAAGGACCT
 TGATGGGCGAGCTAGACTTTGAAGAATTTGTCCATTATCTCCAAGTATCATGAGAAGAGCTGA
 GGCTGCTGTTTAAGATTTTGACAAAAAAGAAATGATGGACGATTGACGGCGAGGAGATCATG
 CAGTCCCTGCGGGGACTTGGGAGTCAAGATATCTGAACAGAGCCAGTGGAGAGACTACCACTCTCC
 CATGGATAAAAAACGGCAGATGACCATCGACTGGAAGCAGTGGAGACATCCACGCTCTCC
 ACCCGTGGAAAAACATCCCGAGATCATCTCTACTGGAAGCATTCACAGTCTTTGATGTG
 GGTGAGAATCTAACGGTCCCGGATGAGTTCACAGTGGAGGAGAGGCAGACGGGGATGTGGT
 GAGACACCTGGTGGCAGGAGGTGGGGCAGGGGCGGTATCCAGAACCTGCACGGCCCCCTGG
 ACAGGCTCAAGGTGCTCATGCAAGGTCCATGCCTCCCGCAGCAACAACTGGGCATCGTTGGT
 GGCTTCACTCAGATGATTCGAGAAGGAGGGGCGAGGTGACCTCTGGCGGGGCAATGGCATCA
 CGTCTCTCAAAATTTGCCCGGAATCAGCCATCAAAATTCATGGCTATGAGCAGATCAAGCGCC
 TTGTTGGTAGTGACCCAGGAGACTCTGAGGATTACGAGCAGGCTTGTGGCAGGCTCTTTGGCA
 GGGGCGATCGCCAGAGCAGCATCTACCAATGGAGTCTTGAAGACCCGGATGGCGCTGGC
 GAAGCAGGCGGACTACTCAGGAATGCTGGACTCGCCAGGAGGATCTGGCCAGAGAGGGGG
 TGGCGGCTTCTACAAAGGCTATGTCCCCAACATGCTGGGCATCATCCCTATGCCGCATC
 GACCTTGCAGTCTACGAGACGCTCAAGAATGCCCTGACAGGCTTGTGGCAGGCTGACAGTGA
 GGACCCCGGGGTGTTTGTGCTCTGGCTGTGGCAGCATGTCCAGTACCTGTGGCCAGCTGG
 CCAGCTTACCCCTGGCCCTAGTCAGGACCCGGATGACGGCCCAAGCCTTATTGAGGCGGT
 CGGGAGGTGACCATGAGCAGCTCTTCAAACTATCTGCGGACCGAGGGGGCTTCGGGCT
 GTACAGGGGGCTGGCCCCCACTTCTATGAGGTTCATCCAGCTGTGAGCATCAGCTCAGTGG
 TCTACGAGAAGCTGAAGATCACTCTGGGCGTGCAGTCTGACGGGGGGAGGGGCGCCCG
 GCAGTGGACTCGCTGATCCTGGGCGCAGGCTGGGGTGTGACCCATCTCATCTGTGAATG
 TGCCAAACACTAAGCTGTCTCGAGCCAGGCTGTGAAAACCTAGACCCACCCCGAGGGAGGT
 GGGGAGAGCTGGCAGGCGCCAGGGCTTGTCTGTGTCACCCAGCAGACCTCTGTTGGTTCC
 AGCGAAGACCAAGGCATTCCTTAGGGTCAGGGTCAGCAGGCTCCGGGCTCAGATGTGTAA
 GGACAGGACATTTTCTGAGTGCCTGCCAATGTGAGCTTGGAGCCTGGAGGCGGCTTAGT
 TCTTCCATTTACCCCTTGACGCGAGCTTTGGCCACGCCCCCTGCCTCTGGTGTCCGCTGC
 ATCTCCCTGTGCCCTCTGTGCTGCCCTGCTGCTGAGGTAAGGTGGAGGAGGGGCTACAG
 CCCACATCCCACCCCTGTGCTCAATGCCATAATCCATGATGAAAGGTGAGGTACGTTGGCT
 CCCAGGCGCTGACTTCCCACTTACAGCATTCAGCCAACTTGGCTGTGAAGGAAGAGGAAAG
 GATCTGGCCTTGTGGTCACTGGCATCTGAGCCCTGCTGATGGCTGGGGCTCTGGGCTATGT
 TGGGAGTGCAGGGGGCTCGGGCTGCCCTGGCTGCACAGAAGCAAGTGTCTGGGCTCA
 TGGTGTCTGAGCTGGCTGGACCTCTCAGATGGGCCCCACCTCAGAACCAAACTCACTG
 TCCCCACTGTGTCATGAGGCGACTGGAGCACCATGTTTGAGGCGGAAGGGCAGGCTTTGT
 GTGTCTGGGGAGGGAAGGAAAAAGGTGTGGAGGCTTAATTAATGACTGTTGGGAAAAGG
 TTTGTCCAGAGGCTAAGCCGACAAATGAGCGACTTCTGTGCTTCCAGAGGAAGCAGG
 GAGCAGGAGCTTGGTCACTGCTCAGAGTCTGTTCTGAGCGCTGGGGGTTCTGTCCAAC
 CCAGCAGGGGCGCAGCGGGAGCAGCCACAGCCCACTTCCACTTGTGCTCACTGTTGGAACCTATT
 ATTTGTATTTATTTGAACAGATTTATGTCTTAATTTTTATAGATTTGTTTAAATTAATA
 GCTGTGATCTTTCAAGTTCAATTTTTATTCAATTTATGTTTATGTTGATTTGATTTGCTTCC
 AAGCCGCCAGTGGGCTGGGAGGAGGAGGAGAAGGGGGGCTTGGGCGCTGCAGTCACT
 CTGTCTCAGAGAAATCTCTTTGGGACTGGAGGCAGAAAAGCGCCAGAGGACAGCAGGACCTG
 GTCCTTCTTTGGCAGTGTGGGAAGGGCTTGCCCCAGCCTTAGGATTTACAGGTTTGA
 CTGGGGGCGTGGAGAGGAGGAGGAACCTCAATAACCTTGAAGTGGAACTCAGGTTATT
 CTGCGTGCAGAGGTTTCTTTATTTCACTCTTTCTGAATGTGAAGTGCAGTGGAGTGGCT
 CACTGTGATGAGTGTGCTGGGCGGGGCTGGAGGAGGGTGGGGGCTGGCTCCGCTCCCTCC
 CAGCTCTGCTGCTGCTTGTCTTAACAAATGCCGGGCCAAGTGGCAGCTCAGGTTGCACTTCC
 ATTCACAGATCACTGATGAGGAATCTCAATAGATGCAAGATCAATGCAAAAAT
 GTTATATATGAACATTAAGTCTGAGTCTGCAAAAAGCAATTAAGAAAGATGGACGTTAG
 AAGTTGTCATTTAAAGCAGCTTCTAATAAGTTGTTTCAAGCTGAAAAAATAAAAAA
 AAAAAA

FIGURE 206

MLCLCLYVPVIGEATFEFYFESKGLPAELKSIFKLSVFIPSQEFSTYRQWKQKIVQAGDKD
 LDGQLDFEEFVHYLQDHEKKRLVFKILDKKNDGRIDAQEI MQSLRDLGVKISEQQAEKILK
 SMDKNGTMTIDWNEWRDYHLLHPVENIPEIILYWKHSTIFDVGENLTVPDEFTVEERQTGMW
 WRHLVAGGGAGAVSRTCTAPLDRLKVLQM VHASRSNNMGIVGGFTQMIREGGARSLWRNGI
 NVLKIAPESAIFEMAYEQIKRLVGSQETLRIHERLVAGSLAGAIQSSIIYPMEVLKTRMAL
 RKTGQYSGMLDCARRILAREGVAAFYKGYVPNMLGIIIPYAGIDLAVYETLKNAWLQHYAVNS
 ADPGVFVLLACGTMSSTCGQLASYPLALVRTRMQAQASIEGAPEVTMSSLFKHILRTEGAFG
 LYRGLAPNFMKVI PAVSISYVVYENLKITLGVQSR

Important features:**Signal peptide:**

amino acids 1-16

Transmembrane domain:

amino acids 284-304, 339-360, 376-394

Mitochondrial energy transfer proteins signature.

amino acids 206-215, 300-309

N-glycosylation site.

amino acids 129-133, 169-173

Elongation Factor-hand calcium-binding protein.

amino acids 54-73, 85-104, 121-140

FIGURE 207

GGAAGGCAGCGGCAGCTCCACTCAGCCAGTACCCAGATACGCTGGGAACCTTCCCCAGCC**AT**
GGCTTCCCTGGGGCAGATCCTCTTCTGGAGCATAATTAGCATCATCATTATTCTGGCTGGAG
 CAATTGCACTCATCATTGGCTTTGGTATTTTCAGGGAGACACTCCATCAGAGTCACTACTGTCT
 GCCTCAGCTGGGAACATTGGGGAGGATGGAATCCTGAGCTGCACCTTTTGAACCTGACATCAA
 ACTTTCTGATATCGTGATACAATGGCTGAAGGAAGGTGTTTTAGGCTTGGTCCATGAGTTCA
 AAGAAGGCCAAAGATGAGCTGTCTGGAGCAGGATGAAATGTTTCAGAGGCCGGACAGCAGTGTTT
 GCTGATCAAGTGATAGTTGGCAATGCCTCTTTGCGGCTGAAAAACGTGCAACTCAGAGATGC
 TGGCACCTACAAATGTTATATCATCACTTCTAAAGGCAAGGGGAATGTAACCTTGAGTATA
 AAACCTGGAGCCTTCAGCATGCCGGAAGTGAATGTGGACTATAATGCCAGCTCAGAGACCTTG
 CGGTGTGAGGCTCCCCGATGGTTCCCCCAGCCCACAGTGGTCTGGGCATCCCAAGTTGACCA
 GGGAGCCAACTTCTCGGAAGTCTCCAATACCAGCTTTGAGCTGAACCTCTGAGAATGTGACCA
 TGAAGGTTGTGTCTGTGCTCTACAATGTTACGATCAACAACACATACTCCTGTATGATTGAA
 AATGACATTGCCAAAGCAACAGGGGATATCAAAGTGACAGAATCGGAGATCAAAGGCGGAG
 TCACCTACAGCTGCTAAACTCAAAGGCTTCTCTGTGTCTCTTCTTTCTTTTGCCATCAGCT
 GGGCACTTCTGCCTCTCAGCCCTTACCTGATGCTAAAA**TAA**TGTGCCTTGGCCACAAAAAAG
 CATGCCAAAGTCATTGTTACAACAGGGATCTACAGAACTATTTACCACCAGATATGACCTAG
 TTTTATATTTCTGGGAGGAAATGAATTCATATCTAGAAGTCTGGAGTGAGCAAAACAGAGCA
 AGAAACAAAAAGAAGCCAAAAGCAGAAGGCTCCAATATGAACAAGATAAATCTATCTTCAA
 GACATATTAGAAGTTGGGAAAAATAATTCATGTGAACTAGACAAGTGTGTTAAGAGTGATAAG
 TAAAATGCACGTGGAGACAAGTGCATCCCCAGATCTCAGGGACCTCCCCCTGCCTGTCACCT
 GGGGAGTGAGAGGACAGGATAGTGCATGTTCTTTGTCTCTGAATTTTTAGTTATATGTGCTG
 TAATGTTGCTCTGAGGAAGCCCCTGGAAAGTCTATCCCAACATATCCACATCTTATATTCCA
 CAAATTAAGCTGTAGTATGTACCCTAAGACGCTGCTAATTGACTGCCACTTCGCAACTCAGG
 GCGGCTGCATTTTAGTAATGGGTCAAATGATTCACTTTTTATGATGCTTCCAAGGTGCCT
 TGGCTTCTCTTCCCACTGACAAATGCCAAAGTTGAGAAAAATGATCATAATTTTAGCATAA
 ACAGAGCAGTCGGGGACACCGATTTTATAATAAACTGAGCACCTTCTTTTAAACAAAAAA
 AA

FIGURE 208

MASLGQILFWSIISIIILAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEPDI
KLSDIVIQWLKEGVLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASLRRLKNVQLTD
AGTYKCYIITSKKGKGNANLEYKTGAFSMPEVNVNDYNASSETLRCEAPRWFPQPTVVWASQVD
QGANSFSEVSNTSFELNSENVTMKVVSVLNVNTINNTYSCMIENDIAKATGDIKVTSEIKRR
SHLQLLNSKASLCVSSFFAISWALLPLSPYMLLK

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FIGURE 209

GAATTTGTAGAAGACAGCGGCGTTGCC**ATG**GCGGCGTCTCTGGGGCAGGTGTTGGCTCTGGT
GCTGTTGGCCGCTCTGTGGGGTGGCACGCAGCCGCTGCTGAAGCGGGCCTCCGCCGGCCCTGC
AGCGGGTTCATGAGCCGACCTGGGCCCAGCAGTTGCTACAGGAGATGAAGACCCCTCTCTTG
AATACTGAGTACCTGATGCCCTTTCTCTCAACCAGTGTGGATCCCTTCTCTATTACCTCAC
CTTGGCATCGACAGATCTGACCTGGCTGTGCCCATCTGTAACCTCTCTGGCTATCATCTTCA
CACTGATTGTTGGGAAGGCCCTTGAGAAGATATTGGTGGAAAACGTAAGTTAGACTACTGC
GAGTGCGGGACGCAGCTCTGTGGATCTCGACATACCTGTGTTAGTTCCTTCCAGAACCCAT
CTCCCCAGAGTGGGTGAGGACACGGCCTTTTCCCATCTGCCCTTTCCTCTGCAGCTGTTTT
GCTTCCTTGTGGCCATCAGAGTTCCCTTCCCCTGGACAGTCTGGAGAAAAGACAGAGGTGGG
GTTTGGGAT**TGA**AGACCAGACCCCATCTGAGCCCTTCTCCAGCCCTGTACCAGCTCCTACT
GGCATGGCTGAGCTCAGACCCTCCTGATTCTGCCTATTATCCAGGAGCAGTTGCTGGCAT
GGTGCTCACCGTGATAGGAATTTCACTCTGCATCACAAGCTCAGTGAGTAAGACCCAGGGC
AACAGTCTACCCCTTTGAGTGGCCGAACCCACTTCCAGCTCTGCTGCCCTCCAGGAAGCCCT
GGGCCATGAAGTGCTGGCAGTGAGCGGATGGACCTAGCACTTCCCTCTCTGGCCTTAGCTT
CCTCCTCTCTTATGGGGATAACAGCTACCTCATGGATCACAATAAGAGAACAGAGTGAAAG
AGTTTTGTAACTTCAAGTGCTGTTGAGCTGCGGGGATTTAGCACAGGAGACTCTACGCTCA
CCCTCAGCAACCTTTCTGCCCCAGCAGCTCTCTTCTGCTAACATCTCAGGCTCCAGCCCA
GCCACCATTACTGTGGCCTGATCTGGACTATCATGGTGGCAGGTTCCATGGACTGCAGAACT
CCAGCTGCATGGAAAGGCCAGCTGCAGACTTTGAGCCAGAAATGCAACGGGAGGCCCTTG
GGACTCAGTCAGAGCGCTTTGGCTGAATGAGGGGTGGAACCGAGGGAAGAAGTGCGTCGGA
GTGGCAGATGCAGGAAATGAGCTGTCTATTAGCCTTGCTGCCCCACCCATGAGGTAGGCAG
AAATCCTCACTGCCAGCCCTCTTAAACAGGTAGAGAGCTGTGAGCCCCAGCCCCACCTGAC
TCCAGCACACCTGGCGAGTAGTAGCTGTCAATAAATCTATGTAACAGACAAAAAAAAAAAA
AAA

FIGURE 210

MAASLGQVLALVLVAALWGQTPLLKRASAGLQRVHEPTWAQQLQEMKTLFLNTEYLMFPFL
LNQCGSLLYYLTASTDLTLAVPICNSLAIIFTLIVKGALGEDIGGKRKLDYCECGTQLCGS
RHTCVSSFPPEPISPEWVRTRPFPILFPFLQFCFLVAIRVPFPWTVWRKTEAGVWD

FIGURE 211

CTTCTGTAGGACAGTCACCAGGCCAGATCCAGAAGCCTCTCTAGGCTCCAGCTTTCTCTGTG
 GAAGATGACAGCAATTATAGCAGGACCTGCCAGGCTGTGAAAAAGATTCCGCAATAAACT
 TTGCCAGTGGGAAGTACCTAGTGAACGGCCTAAGATGCCACTTCTTCTCATGTCCCAGGCT
 TGAGGCCCTGTGGTCCCCATCCTTGGGAGAAGTCAGCTCCAGCACCATGAAGGGCATCCTCG
 TTGCTGGTATCACTGCAGTGCTTGTTCAGCTGTAGAATCTCTGAGCTGCGTGCAGTGTAAT
 TCATGGGAAAAATCCTGTGTCAACAGCATTGCCTCTGAATGTCCCTCACATGCCAACACCAG
 CTGTATCAGCTCCTCAGCCAGCTCCTCTCTAGAGACACCAGTCAGATTATACCAGAATATGT
 TCTGCTCAGCGGAGAACTGCAGTGAGGAGACACACATTACAGCCTTCACTGTCCAGTGTCT
 GCTGAAGAACACTTTCATTTTGTAAAGCCAGTGCTGCCAAGGAAAGGAATGCAGCAACACCAG
 CGATGCCCTGGACCTCCCTGAAGAACGTGTCCAGCAACGCAGAGTGCCCTGCTTGTATG
 AATCTAATGGAACCTCCTGTCTGGGAGCCCTGGAATGCTATGAAGAAGAACAGTGTGTC
 TTTCTAGTIGCAGAACTTAAGAAATGACATTGAGTCTAAGAGTCTCGTGCTGAAAGGCTGTTC
 CAACGTCAGTAACGCCACCTGTGTCAGTTCTGTCTGGTGAAAACAAGACTCTTGAGAGAGTCA
 TCTTTCGAAAGTTTGAGTGTGCAAAATGTAACAGCTTAACCCCCAGTCTGCACCAACCACT
 TCCCACAACGTGGGCTCCAAAGCTTCCTCTACCTCTTGGCCCTTGCCAGCCTCCTTCTTCG
 GGGACTGCTGCCCTGAGGTCTGGGGCTGCACCTTGGCCAGCACCCCATTTCTGCTTCTCTG
 AGGTCCAGAGCACCCCTGCGGTGCTGACACCTCTTTCCCTGCTCTGCCCCGTTTAACTGC
 CCAGTAAGTGGGAGTCACAGGTCTCCAGGCAATGCCGACAGCTGCCTTGTCTTCAATTATTA
 AAGCACTGGTTCATTCAGTCCAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 212

MKGILVAGITAVLVAAVESLSVCVQCSWEKSCVNSIASECPSHANTSCISSASSSLETVPV
 LYQNMFCSAENCSEETHITAFTHVHSAEEHFHVFSQCQKGKCSNTSDALDPPLKNVSSNAE
 CPACYESNGTSCRGPWKCYEEEQCVFLVAELKNDIESKSLVLKGCSNVSNATCQFLSGENK
 TLGGVIFRKFECAVNSLTPTSAPTTHNVGSKASLYLLALASLLLRGLLP

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FIGURE 213

GGCCTCGGTTCAAACGACCCGGTGGGTCTACAGCGGAAGGGAGGGAGCGAAGGTAGGAGGCA
 GGGCTTGCCCTCACTGGCCACCCCTCCCAACCCCAAGAGCCAGCCCCATGGTCCCCGCCGCCG
 GC GCCTGCTGTGGGTCTGCTGCTGAATCTGGGTCCCCGGCGGGGGGCCAAGGCCCTG
 ACCCAGACTCCGACCGAAATGCAGCGGGTCAGTTACGCTTTGGGGGCCCCATGACCCGCAG
 CTACCGGAGCACGCCCCGGACTGGTCTTCCCGGAAGACAAGGATAATCCTAGAGGACGAGA
 ATGATGCCATGGCCGACGCCGACC GCCTGGCTGGACCAGCGGCTGCCGAGCTCTTGGCCGCC
 ACGGTGTCCACCGGCTTTAGCCGGTCTGCCCCATTAAACGAGGAGGATGGGTCTTCAGAAGA
 GGGGTTTGTGATTAATGCCGGAAGGATAGCACCAGCAGAGAGCTTCCAGTGC GACTCCCA
 ATACAGCGGGGAGTTCCAGCACGAGGTTTATAGCCAATAGTCAGGAGCCTGAAATCAGGCTG
 ACTTCAAGCCTGCCGCGCTCCCCGGGAGGTCTACTGAGGACCTGCCAGGCTCGCAGGCCAC
 CCTGAGCCAGTGGTCCACACCTGGGTCTACCCCGAGCCGGTGGCCGTCACCCTCACCCACAG
 CCATGCCATCTCCTGAGGATCTGCGGCTGGTGCTGATGCCCTGGGGCCCGTGGCACTGCCAC
 TGCAAGTCGGGCACCATGAGCCGAGCCGGTCTGGGAAGCTGCACGGCCTTTCCGGGCGCCT
 TCGAGTTGGGGCGCTGAGCCAGCTCCGCACGGAGCACAAAGCCTTGACCTATCAACAATGTC
 CCTGCAACCGACTTCGGGAAGAGTGCCCCCTGGACACAAGTCTCTGTACTGACACCAACTGT
 GCCTCTCAGAGCACCACCAGTACCAGGACCACCCTACCCCTTCCCCACCATCCACCTCAG
 AAGCAGTCCCAGCCTGCCACCCGCCAGCCCTGCCAGCCCTGGCTTTTGGAAACGGGTCA
 GGATTGGCTGGAGGATATTTGGAATAGCCTCTCTTCAGTGTTACAGAGATGCAACCAATA
 GACAGAAACCAGAGGTAAATGGCCACTTCATCCCATGAGGAGATGTGAGTATCTCAACCTCT
 CTTGCCCTTTCAATCCTAGCACCCACTAGATATTTTTAGTACAGAAAAACAAACTGGAAAA
 CACAA

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FIGURE 214

MVPAAGALLWVLLNLGPRAAGAGLTQTPTEMQRVSLRFGGPMTRSYRSTARTGLPRKTRI
ILEDENDAMADADRLAGPAAELLAATVSTGFSRSSAINEEDGSSEEGVVINAGKDSREL
PSATPNTAGSSSTRFIANSQEPEIRLTSSLPRSPGRSTEDLPGSQATLSQWSTPGSTPSRWP
SPSPTAMPSPEDLRLVLPWGPWHCHCKSGTMSRSRSGKLHGLSGRLRVGALSQLRTEHKPC
TYQQCPCNRLREECPLDTSLCDTNCASQSTTSTRTTTTPFPTIHLRSSPSLPPASPCPALA
FWKRVIRIGLEDIWNSSLSSVFTEMQPIDRNQR

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CCGGGCTGCACACACCGGCTGGGGGAGAGCAATGGTCGGCGCTGGCGGCGCGGTGGTCTGCTGATGGGGCA
CGCGCTGGGACGGCGCTCCAGGGGACGCTGAGCGGTGACCGCACTGCTACGCTACGCTACGATGCGAAGAGCA
GAACCTGCTCTGGGGCGGCTCTGAATCACTTCGCGTCCGCGCAGCAAACTACATGACTCTAGACGGCTGACCT
CTCGGACGACTGTAAATGATGATGTATGTGGGTACCGCTGTGGGCTCTACCTCCAGAAAGTCAAAAGTGCCCT
CAGTTCATGSCAGATGGCCCTTCTCCGGTTCTCTTTTTCAGAGCGCGGACCTCGGCCGTGGCTCTGTTTCT
CAATGGCCTGGCCACGCTGGTGATGCTCTCGCGCTACGCCACGCTCTGTCGCGAGCCTCTCTCCCCATGTACCA
CTTGCTGGCTGCTGCTGGCTGGTGGCTTCAATGATCGTTGTGTCGCACAGTCTTCCACACAGGGACACTGA
CTGCACAGAGAAATGGACTACTCTTGCTGCTCCACTGCTACTCATCACTCAATCACTCTGTTGGCTCGAGCAG
CTGGGGCTCGAGCAACCGAGCTGGTGTCAGTGGCTCTCCGGGCTCTCTGCTGCTAGCTGACCTGACGTGCAGCTCT
CTTACTCGAGCTCACTCCGCTCTGCAATGAGCTGCTACCACTGCTGGGACAGCGGCTATGGGCTGGTCAAGTGT
GTGGTGGGCTGGGCTGGGCTCGTGGAAACCAAGCGCGCGTGCCTACGTCGCGCAAGTGGCTGGTGGTGGCTTGT
GCTGCTGCAGGGGGTCTCCCTCTCGAGCTGCTTGACTTCCACGCTCTTCTGGGCTCTGGATGCCCATGCCA
TCTGGCAATCAGACATCACTCCCTGACAGTCTCTTTTACAGCTTCTCGAAGATGACACCTGACTGCTGTG
AAGAAATCAGAGGACAGTTCAGCTGAGCACTGAAGATCTGAGGCGGCTCGGCCAGTGGGGATCTGCCGCC
GCCCTGGTGGGCTCCCTTCTCCCTCAACCTTGAGATGATTTTGGTCTTTTCAACTTTTGAATTGGACATGA
AGGATGGTGGGCGAAGATCAGTGGCGAGCCCAACCCCTTTGACCTCTCAGACGCTTGGAGTCTGTTCTTAGG
AAGCCCTCCAGCATCTGGAGCTCGAGAGTGGGCAAGCCCTCTGCCCTCTGAGCTGAACTGGGGTGGAACTGA
GTGTGTTCTTAGCTCTACCGGAGAGACAGCTGCTGTTTCTCCACACAGGCTCTCTCCCATCTCCCGAGCTG
CTGGCTGGGCTCGAAGAGCTCTGTGCTACTCTGAGGACAGGAGCAACAGGCTCTAGGGAACAGAGGGGCTCC
CTTCTGTTACACACCCCACTCCCTCTCCAGGACACCACTAGTGGTGTGCTGGATGTTGTCTTTTGGCGAGCCACA
GGTTACGGCGAGTCTCCCATGGGATCTTGAGGAGCAAGCTGCTGGGATGGGAAGAGGATTTACCTGACC
GTTGGCTTACGCAAGTTCAGAGGAGCTCCACCACTCCCTTTCCAGGCGAGGCTCCAGCAGCGCCAGGCA
AGGATCTTGCTGCTGCTGTGTGTGAGAGCTGCCACCTGTGTGCGGAGTGTGGGCAAGCTGAGTGCTATAG
TGACAGAGGCGCTGAGCATGGGCTGGGTTGTGTGAGCTCAGGCTAGGTCGGCATGTGGAGACGGGTGTTGT
CGGGAGAGGAGTGTTGGCTTCAAAGTGTGTGTGTGTCAGGGGGTGGGTTGTTAGCTGGGTGAGGGGAAGCTGT
TGCGCTGCTGTGGGGATGTGAGATGAGTACTGCGGCTGAATGTGTGCCAAGTTGAGAGTTGTGAGCAGAT
GAGGGAATCTGTGCACATCAATTAATCACTTGTGGAGCGGACAGCTCTGCCAAGACGCCACCTGGGCGACAGC
CAGAGGCTCTCCATGGCCAGCTGCCCTGTGTGATGTTCCTCTGTGTGCGCCTTTGCCGCTCTCTGCATCA
CTCACAGGTTCCCAACAACAGTGGCTGTGCAGAACGAGCCCTCGAAGGACAGGAAGAAGAAATGGGATGGC
TGGGCGCTCTCTCATCTCTCTTTCTCTGCTGCTGCTGCATGAGGCTGGGCTCTCCCTCCAAACACTCTATCTCCCT
GTGTCAGCGCCTTTGCCATAGCTGATTTTGGGAGAGGAGGAAGGGCGCATTTGAGGAGAGAGGGAAGAAAGCT
TATGGCTGGGTCTGGTTTCTTCTCCCTCCGAGAGGTTCTACTGTCTCAGGTTGGGCCCGGACGAGGCGAGGCGC
ACACTATGCTCTGGCTGTGAAGAGTGACCCCTGCATTTACGACAGCCCTGGCATGTCTCTGCCACAGG
AATGAGATGGAGGAGCTCGCAAACTTTTCATCCCAAGGCAAGCTCTCCGTTGTGAAGCAGACTGGATTTTTC
CTCTGCCCTACCCCTTGPCCCTTTGAGGAGGGGAGCTATGCTAGGACTCAACCTCAGGACTCGGGTGT
GCTCGGCTAGCTCTTTTGTATCACTAAACCTTTAAGTGGGAGGTTGGCAGGAGTGTGCTTAATAATCAA
TTCCAGACTCTCAAAAAGAAAAA

FIGURE 216

MAGLAARLVLLAGAAALASGSQGDREPVYRDCVLQCEEQNCSGGALNHFRSRQPIYMSLAGW
TCRDDCKYECMWVTVGLYLQEGHKVPQFHGKWPFSSRLFFQEPASAVASFLNGLASLVMLCR
YRTFVPASSPMYHTCVAFAWVSLNAWFWSTVFHTRDTDLTEKMDYFCASTVILHSIYLCCVR
TVGLQHPAVVSAFRALLLLMLTVHVSYSLSLIRFDYGYNLVANVAIGLVNVVWWLAWCLWNQR
RLPHVRKCVVVVLLQLGLSLELLDFPPLFWVLDAAHAIWHISTIPVHVLFSSFLEDDSLYLL
KESEDKFKLD

Important features:**Signal peptide:**

amino acids 1-20

Transmembrane domains:

amino acids 105-123, 138-156, 169-185, 193-209, 221-240, 256-272

N-glycosylation site.

amino acids 40-44

N-myristoylation site.

amino acids 43-49

CUB domain proteins profile.

amino acids 285-302

Amiloride-sensitive sodium channels proteins.

amino acids 162-186

[illegible]

FIGURE 218

MAPQSLPSSRMAPLGMLLGLLMAACFTFCLSHQNLKEFALTNPESSTKETERKETKAEEL
 DAEVLEVHPTHEWQALQPGQAVPAGSHVRLNLQTGEREAKLQYEDKFRNNLKGRDLINTN
 TYTSQDLKSALAKFKEGAEMESSKEDKARQAEVKRLFRPIEELKKDFDELNVVIETDMQIMV
 RLINKFNSSSSSLEEKIAALFDLEYVHVHMDNAQDLLSFGGLQVVINGLNSTEPVKEYAAF
 VLGAAFSSNPVKVQVEAIEGGALQKLLVILATEQPLTAKKKVLFALCSLLRHFPYAQRQFLKL
 GGLQVLRITLVQEKGEVLAVRVVTLTYDLVTEKMFEEEEAELTQEMSPEKLQQYRQVHLLPG
 LWEQGWCEITAHLLALPEHDAREKVLQTLGVLLTTCRDRYRQDPQLGRTLASLQAEYQVLAS
 LELQDGEDEGYFQELLGSVNSLLKELR

Important features:**Signal peptide:**

amino acids 1-29

Hypothetical YJL126w/YLR351c/yhcX family protein.

amino acids 364-373

N-glycosylation site.

amino acids 193-197, 236-240

N-myristoylation site.

amino acids 15-21, 19-25, 234-240, 251-257, 402-408, 451-457

Homologous region SLS1 protein.

amino acids 68-340

FIGURE 219

TTCGGCTTCCGTAGAGGAAGTGGCGCGGACCTTCATTTGGGGTTTCGGTTCCCCCCCCCTCC
 CTCCCCGGGGTCTGGGGGTGACATTGCACCGCGCCCTCGTGGGGTCGGTGTGCCACCCCA
 CGCGGACTCCCCAGCTGGCGCGCCCCCTCCATTGGCTGTCTGGTCAGGCCCCACCCCC
 TTCCCACCTGACCAGCCATGGGGGCTGCGGTGTTTTTCGGCTGCACCTTCGTGCGGTTCGGC
 CCGGCTTCGCGCTTTTCTTGATCACTGTGGCTGGGACCCGCTTCGCGTTATCATCTCGGT
 CGCAGGGGCATTTTCTGGCTGGTCTCCCTGCTCCTGGCCCTCTGTGGTCTGGTTTCATCTTGG
 TCCATGTGACCGACCGGTGAGATGCCCGGCTCCAGTACGGCCCTCCTGATTTTGGTGTCTGCT
 GTCTCTGTCTTCTACAGGAGGTGTTCCGCTTTGCCTACTACAAGCTGCTTAAGAAGGCAGA
 TGAAGGGTTAGCATCGCTGAGTGAGGACGGAAGATCACCACTCTCATCCGCCAGATGGCCT
 ATGTTTCTGGTCTCTCCTTCGGTATCATCAGTGGTGTCTCTCTGTTATCAATATTTTGGCT
 GATGCACTTGGGCCAGGTGTGGTGGGATCCATGGAGACTCACCTTATTACTTCTGACTTC
 AGCCTTCTGACAGCAGCCATTATCCTGCTCCATACCTTTTGGGGAGTTGTGTTCTTTGATG
 CCTGTGAGAGGAGACGGTACTGGGCTTTGGGCCCTGGTGGTGGGAGTCACCTACTGACATCG
 GGACTGACATTCTGAAACCCCTGGTATGAGGCCAGCCTGCTGCCCATCTATGCAGTCACTGT
 TTCCATGGGGCTCTGGGGCTTTCATCACAGCTGGAGGGTCCCTCCGAAGTATTAGCGCAGCC
 TCTTGTGTAAGGACTGACTACCTGGACTGATCGCTGACAGATCCACCTGCCTGTCCACTG
 CCCATGACTGAGCCAGCCCCAGCCGGGTCCATTGCCACATCTCTGTCTCCTTCTCGTC
 GGTCTACCCCACTACCTCCAGGGTTTGTCTTTGTCTTTTGTGACCGTTAGTCTCTAAGCTT
 TACCAGGAGCAGCCTGGGTTCAGCCAGTCACTGACTGGTGGGTTTGAATCTGCACTTATCCC
 CACCACCTGGGGACCCCTTGTGTGTCTCCAGGACTCCCCCTGTGTGCTGCTGTCTGCTCTC
 CCTGCCCAAGACTCACCTCCCTTCCCTCTGCGAGGCCAGCGCAGGAGGACAGTCGGGTGAT
 GGTGTATCTGCCCCTGCGCATCCACCCGAGGACTGAGGGAACCTAGGGGGGACCCCTGGGC
 CTGGGGTGCCCTCCTGATGTCTCGCCCTGTATTCTCCATCTCCAGTTCTGGACAGTGACG
 GTTGCCAAGAAAAGGACCTAGTTTAGCCATTGCCCTGGAGATGAAATTAATGGAGGCTCAA
 GGATAGATGAGCTCTGAGTTTCTCAGTACTCCCTCAAGACTGGACATCTTGGTCTTTTCTC
 AGGCCTGAGGGGGAACCATTTTGGTGTGATAAATACCCTAACTGCCTTTTTTCTTTTTT
 GAGGTGGGGGAGGAGGAGGTATATGGAACCTCTTAACCTCCTTGGGCTATATTTCTC
 TCCTCGAGTTGCTCTCATGGCTGGGCTCATTTCCGTTCCCTTTCTCCTTGGTCCAGACCTT
 GGGGGAAGGAAGGAGTGCATGTTTGGGAACGGCATTACTGGAACATAATGTTTTAACCT
 CCTTAACCACCAGCATCCCTCCTCTCCCCAAGGTGAAGTGGAGGGTGTGTGGTGAGCTGGC
 CACTCCAGAGCTGCAGTGCCACTGGAGGAGTCACTACCATGACATCGTAGGGAAGGAGGG
 GAGATTTTTTGTAGTTTTTAATTTGGGGTGTGGGAGGGCGGGGAGGTTTTCTATAAAGCT
 ATCATTTTCTGCTAGGGTGGAGTGTCCCATCCTTTAATCAAGGTGATTGTGATTTGACT
 AATAAAAAAGAAATTTGTAAAAA
 AA

FIGURE 220

MGAAVFFGCTFVAFGPAFALFLITVAGDPLRVIIILVAGAFFWLVSLLLASVVWFILVHVTDR
SDARLQYGLLIFGAAVSVLLQEVFRFAYYKLLKKADEGLASLSEdGRSPISIRQMAYVSGLS
FGIISGVFSVINILADALGPGVVGIIHGDSPIYFLTSAFLTAAILLHTFWGVVFFDACERRR
YWALGLVVGSHLLTSGLTFLNPWYEASLLPIYAVTVSMGLWAFITAGGSLRSTQRSLCKD

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AAGCTGGTTTAAAGGAAGCAGAGGAGGGTTAGATTCGTTGAGTGAGGACGGAAGATCAACCCA
 TTTCCATTCCGCCAGATGGCCTATGTTTCTGGTCTCTCCCTTCGGNATCATCAGTGGTGTNT
 TNTCTGTTATCAATATTTTGGCTGATGCANTTGGGCCAGGTGTGGTTGGGATCCATGGAGAC
 TCACCCATTANTTCCGTGANTTCAGCCTTTNTGACAGCAGCCATTATCCTGCTC

GACCGACCGTTTCAGATGCCCGGTTCCAGTACGGCTTCTGATTTTTGGTGTCTGCTGTNTCTG
TCCTTCTACAGGAGGTGTTCCGCTTTGCCTANTACAAGCTGCTTAAGAAGGCAGATGAGGGG
TTAGCATNCTGAGTGAGGACGGAAGATCACCATTTCATCCGCCAGATGGCCTATGTTTN
TGGTNTTTCCTTCGGTATCATCAGTGGTGTTTTNTCTGTTATCAATATTTTGGNTGATGCAN
TTGGGCCAGGTGTGGTTGGGATCCATGGAGANTCACCCTATTAATTCTGAATTCAGCCTTT
NTGACAGCAGCCATTATCCTGNTCCATACCTTTTGGGGAGTTGTGTTTTTGTATGCCTGTGA
GAGGAG

NGTTGGAGAAGTGGCGCGGACNNTTCATTGGGGTTTCGGTTTCCCCCTTCCCTTTCCCGG
GGGTCTGGGTGACATTGCACGGGCCCTCGTGGGTGCGGTGCCACCCACGCGGACTCC
CCAGNTGGNGCGCCTTCCCAATTGCCTGTCTGGTCAGGCCCCACCCCTTCCACNTG
ACCAGCCATGGGGCTGCGGTGTTTTTCGGCTGCACTTTCGTGCGTTGCGCCCGGCCTTCG
CGCTTTTCTTGATCACTGTGGCTGGGGACCGCTTCGCGTTATCATCTGTGTCGAGGGCA
TTTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTATCTTGGTCCATGTGAC
CGACCGGTGAGATGCCCGGCTCCAGTACGGCCTCCTGATTTTTGGTGCTGCTGTCTCTGTCC
TTCTACAGGAGGTGTTCCGCTTTCCTACTACAAGCTGCTTAAGAAGGCAGATGAGGGGTTA
CATCTGCTAGTGAGGACGGGAAGATACCCCATCTCCATCCGCCAGATGGCCTATGTTTCTGG
TCTCTCCTTCGGTATCATGATCGTGGTGTCTTCTCTGTTATCAATATTTGGCTGATGCACCTG
GGCCAGGTGTGGTTGGGATCCATGGAGACTACCC

FIGURE 224

GTAAAAGAAAGTGGCCGGACCTTCATTGGGGTTTCGGTTCCTCCCTTTCCCNNTTCCCCGGGG
TCTGGGGGTGACATTGCACCGCGCCCNCTCGTGGGGTCGCGTTGCCACCCACGCGGACTCCC
CAGNTGGCGCGCCCTCCCATTTGCCGTGTCTGGTCAGGCCCCACCCCTTCCCACCTGA
CCAGCCATGGGGGCTGCGGTGTTTTTCGGGCTGCACTTCGTGCGGTTTCGGGCCCGGCTTC
GCGCTTTTCTTGATCACTGTGGCTGGGGACCGCTTCGCGTTATCATCTGGTCGCAGGGGC
ATTTTTCTGGCTGGTCTCCCTGCTCCTGGCTCTGTGGTCTGGTTCATCTGGTCCATGTGA
CCGACCGGTGAGATGCCCGGCTCCAGTACGGCTCCTGATTTTTGGTGCTGTCTCTGTCTGTC
CTTCTACAGGAGGTGTTCCGCTTTCCTACTACAAGCTGCTTAAGAAGGCAGATGAGGGGTT
AGCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCCAGATGGCCTATGTTTCTG
GTCTCTCCTTCGGTATCATCAGTGGTGTCTTCTCTGTTATCAATATTTGGCTGATGCACTT
GGGCCAGGTGTGGTTGGGATCCATGGAGAC

FIGURE 225

GCCCCAGGGAGCAGTGGGTGGTTATAACTCAGGCCCGGTGCCAGAGCCCAGGAGGAGGCAG
 TGCCAGGAAGGCACAGGCCCTGAGAAGTCTGCGGCTGAGCTGGGAGCAAATCCCCACCCCC
 TACCTGGGGGACAGGGCAAGTGAGACCTGGTGAGGGTGGCTCAGCAGGCAGGGAAGGAGAGG
 TGCTGTGCGCTCCTGCACCCACATCTTTCTCTGTCCCTCCTTGCCCTGTCTGGAGGCTGCT
 AGACTCCTATCTTCTGAATTCTATAGTGCCTGGGTCTCAGCGCAGTGCCGATGGTGGCCCGT
 CTTGTGGTTTCCTCTCTACCTGGGGAATAAGGTGCAGCGGCC**ATGG**GCTACAGCAAGACCCC
 CCTGGATGTGGGTGCTCTGTGCTCTGATCACAGCCTTGCTTCTGGGGGTACAGAGCATGTT
 CTCGCCAACAAATGATGTTTCTGTGACACCCCTCTAACACCGTGCCCTCTGGGAGCAACCA
 GGACCTGGGAGCTGGGGCCGGGAAGACGCCCGGTGGATGACAGCAGCAGCCGCATCATCA
 ATGGATCCGACTGCGATATGCACACCCAGCCGTGGCAGGCCGCGCTGTTGCTAAGGCCAAC
 CAGCTCTACTGCGGGGCGGTGTGGTGCATCCACAGTGGCTGCTCAGGCCGCCCACTGCAG
 GAAGAAAGTTTTCAGAGTCCGTCTCGGCCACTACTCCCTGTACCAGTTTATGAATCTGGGC
 AGCAGATGTTCCAGGGGGTCAAATCCATCCCCACCCCTGGCTACTCCACCCCTGGCCACTCT
 AACGACCTCATGCTCATCAAAGTGAACAGAAGAATTGCTCCCACTAAAGATGTCAGACCCAT
 CAACGTCTCCTCTCATTTGTCCTCTGCTGGGACAAAGTGCTTGGTGTCTGGCTGGGGGACAA
 CCAAGAGCCCCCAAGTGCACTTCCCTAAGGTCTCCAGTGCTTGAATATCAGCGTGCTAAGT
 CAGAAAAGGTGCGAGGATGCTTACCCGAGACAGATAGATGACACCATGTTCTGCGCCGGTGA
 CAAAGCAGGTAGAGACTCCTGCCAGGGTGATTCTGGGGGCGCTGTGGTCTGCAATGGCTCCC
 TGCAGGGACTCGTGTCTGGGGAGATTACCTTGTGCCCGGCCAACAGACCGGGTGTCTAC
 ACGAACTCTGCAAGTTACCAAGTGGAATCCAGGAAACCATCCAGGCCAACTCT**TGAG**TCAT
 CCCAGGACTCAGCACACCGGCATCCCCACCTGCTGCAGGGACAGCCCTGACACTCCTTTACG
 ACCCTCATTCCTTCCCAGAGATGTTGAGAATGTTCTCTCTCCAGCCCTGACCCCATGTCT
 CCTGGACTCAGGGTCTGCTTCCCCACATTGGGCTGACCGTGTCTCTAGTTGAACCCTGG
 GAACAATTTCCAAAAGTGTCCAGGGCGGGGGTGGCTCTCAATCTCCCTGGGGCACTTTTCAT
 CCTCAAGCTCAGGGCCATCCCTTCTCTGCAGCTCTGACCCAAATTTAGTCCAGAAATAAA
 CTGAGAAGTGAAAAA

FIGURE 226

MATARPPMMWVLCALITALLGVTEHVLANNVSCDHPSNTVPSSGNQDLGAGAGEDARSDD
SSSRIINGSDCDMHTQPWQAALLLRPNQLYCGAVLVHPQWLLTAAHCRKKVFRVRLGHYSLS
PVYESGQQMFQGVKSIHPHPGYSHPGHSNDLMLIKLNRIRPTKDVRPINVSSHCPASGATKCL
VSGWGTTKSPQVHFPKVLQCLNISVLSQKRCEDAYPRQIDDTMFCAGDKAGRDSCQGDSSGGP
VVCNGSLQGLVSWGDP CARPNRPGVYTNLCKFTKWIQETIQANS

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FIGURE 227

ATGTGTC AACGACCGGTGGAAGACCATGGGCGGCGCTGCCAACTTGAGGACCGGCCGCGCGA
 CAAGCCGACGCGGCCGAGCTGCGGGTACGTGCTGTGCACCGTGTGCTGTGGCCCTGGCTGTGC
 TGCTGGCTGTAGCTGTACCGGTGCCGTGCTCTTCCGAAACACGCCACCGCCGCGGGGACG
 GCGGCCCACTGTGCTGAGCACTGGGGCTGCCAGCGCCAACAGCGCCCTGGTCACTGTGGA
 AAGGGCGGACAGCTCGCACTCAGCATCTCATTTGACCGCGCTGCCCGACCTCAGGCACA
 GCTTCGCAAGCGCTGGAGAGCGCCAGGCCCTCGTGTGTCAGGCGCTGCACAGACACCAAGGCG
 CAGCCACGGCTGTGGGCGACAGGAGCAGGAGCTGCTGGACAGCTGGCCGACCAAGCTGCC
 CGGGCTGTGTGGCCGAGCCTCAGAGCTGCAGACGGAGTGCATGGGGCTGCGGAAGGGGCATG
 GCACGCTGGGCGAGGGCTCAGCGCCCTGCAGAGTGAGCAGGGCGCCCTCATCCAGCTTCTC
 TCTGAGAGCCAGGGCCACATGGCTCACCTGGTGAACCTCCGTCAGCGACATCCTGGATGGCCT
 GCAGAGGGACCGGGGGCTGGGCGGCCCCGCAACAAGGCCGACCTTCAGAGAGCGCCTGCC
 GGGGAACCCCGGCCCGGGGCTGTGCCACTGGCTCCGGGCCCGAGACTGTCTGGACGTCTCT
 CTAAGCGGACAGCAGGACGATGGCGTCTACTCTGTCTTTCCCACTCATCCCGCGCGGCTT
 CCAGGTGTACTGTGACATGCGCACGGACGGCGCGGCTGGACGGTGTTCAGGCGCGGGAGG
 ACGGCTCCCGTGAACCTTCTCCGGGGCTGGGACGCTACCGAGACGGCTTTGGCAGGCTCAC
 GGGGAGCACTGGCTAGGGCTCAAGAGGATCCACGGCTGACCACACAGGCTGCCTAGAGCT
 GCACGTGGACCTGGAGGACTTTGAGAATGGCACGGCTATGCCGCTACGGGAGCTTCGGCG
 TGGGCTTGTCTCCGTGGACCTTGAGGAAGACGGGTACCCGCTCACCGTGGCTGACTATTCC
 GGCATCTCAGGCGGACTCCTCCTGAAGCACAGCGGCATGAGGTTTACCCAAAGGACCGTGA
 CAGCGACCATTCAGAGAACAACCTGTGCGCCCTTCTACCGGCTGCTGTGGTACCGCAACT
 GGCACAGCTCAAGCTCAATGGGAGTACCTGCGCGGTGCCACGCTCTCATGCCGACGGC
 GTGGAGTGGTCCCTCTGGACCGGCTGGCAGTACTACTCAAGTCTCTGAGATGAAGATCCG
 GCGGGTCCGGGAGGACCGCT**TAG**ACTGGTGCACCTTGCTTGGCCCTGCTGGTCCGTGCG
 CCCATCCCCGACCCACCTCACTCTTTCGTGAATGTTCTCCACCCACCTGTGCTGGCGGAC
 CCACTCTCAGTAGGGAGGGGCGGGCCATCCCTGACACGAAGCTCCCTGGCGCGGTGAAGT
 CACACATCGCTTCTCGCCGTCCCGACCCCTCCATTTGGCAGCTCACTGATCTCTTGCTCT
 TGCTGATGGGGCTGGCAAACCTTGACGACCCCACTCTGCTGCCCGCACTGTGACTCCGG
 TGCTGTTGGCGCTCCCTGTGGCAGGATGCTGGAGCTGTGCCCGAGGACCTCTGCGCTGCC
 TGCCAAATACCCGGCATTTGGGGACAGAGAGCAGGGGGCAGACGACCCCTGGAGTCTCTC
 CTAGCAGATCGTGGGGAATGTCAAGTCTCTCTGAGGTGAGGTCTGAGGCCAGTATCCTCCAG
 CCTCCGAATGAGCAACCCGACCTCGTTTCCCTGGTGCCCAAGAGAACCCACCTCTGCCCAA
 GGGCCTCAGCGCTGGCTGTGGGCTGGGTGGCCCATCTACAGGCGCTGAGGTCAAGATGGG
 GAGCTGTGCTTTGGGGACCCACGCTCCAAGGTGAGACAGTTCCCTGGAGGCCACCCAC
 CTTGTGCCCGGCGAGGCTGGGGTGTGCAGTCTCTTACCTGTCTGTGCCACCTGTCTCTGT
 TCTCAAATGAGGGCCAAACCCATCCCCACCCAGCTCCCGGCGTCTCCTACTCGGGCAGC
 CGGGGCTGCCATCCATTTCTCCTGCCCTGGAAGGTGGGTGGGGCCCTGCACCGTGGGGCT
 GGAGTCGCTAATGGGAAGCTCTTGGTTTTCTGGGCTGGGGCTAGGCAGGGCTGGAGATGAG
 GCTTGTACAAACCCCAACCAATTTCCAGGGACTCCAGGGTCTGAGGCTCTCCAGGAGG
 GCTTGTGGGCTGATGACCTTCCCTGAGGTGGCTGTCTTCTGAGGAGGCCAACCTTGCTTCC
 ATTGACCGTGGCCACCTGGACCCAGGCCAGGCCCGGGCCCGCGAGTGGTCAAGGGACAGGGA
 CCACTCACCGGCCAAATGGGGTGGGGGGACTGGGGCACCAGACAGGACCACTGGACA
 CTTTCTGTGTGAATCTTCCCAACCCAGCACGCTGTATCCCACTCCTTGTGTGCACACA
 TGTACGCTGAGACCCGAGGCTCCAGGACAGCAGGCCAAGGGCAGGCGCTGGAGCCGGG
 TCTCAGCTGTCTGTCTCAGCAGCCTTGGACCCGCGTGCCTTACGTGAGGCCAGATGACAGG
 CGGCTTTTCCAAGGCTTCTGTATGGGGGCTCCGAAGGGCTGGATGAGCTGAGCTTGGGAGCT
 GCCTAGCAGCTCTCTCTGGGCGAGGAGGGGAGGTGGCTTCTCCTCAAAGGACACCCGATGGCA
 GGTGCTACGGGGTGTGGGGTTCGGTTCTCCCTTCCCTCCCAAGTTTGTGCTTAAAA
 AACATAAATTTGACTTGGCACCACTGGGGTGGTGGGAGAGGCGGTGTGACCTGGCTCTC
 GTCCAGTGCACCAAGGTCATCCACATGCGGAG

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FIGURE 228

MVNDRWKTMGGAAQLED RPRDKPQRPS CGYVLCTVLLALAVLLAVAVTGAVLFLNHAHAPGT
APPPVVSTGAASANSALVTVERADSSHLSILIDPRCPDLTDS FARLESAQASVLQALTEHQA
QPRLVGDQE QELLDTLADQLPRL LARASELQTECMGLRKGHGTLGQGLSALQSEQGR LIQLL
SESQGHMAHLVNSVSDILDALQRDRGLGRPRNKADLQRA PARGTRPRGCATGSRPRDCLDVL
LSGQQDDGVYSVFP THYPAGFQVYCDMRTDGGGWTVFQRREDGSVNFFRGWDAYRDGFGRLT
GEHWLGLKRIHALTTQAAYELHVDLED FENG TAYARYGSFGVGLFSVDPEEDGYPLTVADYS
GTAGDSL LKHSGMRFTTKDRDS DHSENNCAAFYRGAWWYRNCHTSNLNGQYLRGAHAS YADG
VEWSSWTGWQYSLKFSEM KIRPVREDR

FIGURE 230

MQAKYSSTRDMLDDGDTTMSLHSQASATTRHPEPRRTEHRAFSSTWRPVALTLLTLCIVLL
IGLAALGLLFFQYYQLSNTGQDTISQMEERLGNTSQELQSLQVQNIKLAGSLQHVAEKLCRE
LYNKAGAHRCSPCTEQWKWHGDNCYQFYKDSKSWEDCKYFCLSENSTMLKINKQEDLEFAAS
QSYSEFFYSYWTGLLRPD SGKAWLWMDGTPFTSELFHIIIDVTSRPRDCVAILNGMIFSKD
CKELKRCVCERRAGMVKPESLHVPPETLGEGD

FIGURE 231

AATTTTCACCGCTGTAGGAATCCAGATGCAGGCCAAGTACAGCAGCACGAGGGACATGNTGG
ATGATGATGGGACACCACCATGAGCCTGCATTNTCAAGCTTTTGCCACAATTCGGCATCCAG
AGCCCCGGCGCACAGAGCACAGGGNTCCTTTTTCAACGTGGCGACCAGTGGCCCTGACCCCTG
CTGACTTTGTGCTTGGTGCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTTCAGTA
CTACCAGCTCTCCAATACTGGTCAAGACACCATTCTCAAATGGAAGAAAGATTAGGAAATA
CGTCCCAGAGTTGCAATTTNTTCAAGTCCAGAATATAAAGCTTGCAGGAAGNTGCAGCAT
GTGGCTGAAAAACTCTGTCGTGAGCTGTATAACAAAGCTGGAGGAACTTTGAAGGAGGGCAA
AGTNTCCTCATNTACTATACACACCACTTCCC

FIGURE 232

GCGGAGCGCAAGAACCCCTGCGCAGCCAGAGCAGCTGCTGGAGGGGAATCGAGGCGCGGCTC
 CGGGGATTGCGGCTCGGGCCGCTGGCTCTGCTCTGCGGGGAGGGAGCGGGCCCCGCCGCGGGG
 CCGGAGCCCTCCGGATCCGCCCTCCCGGCTCCCGCCCCCTCGGAGACTCCTCTGGCTGCT
 CTGGGGGTTCCGCCGGGGGACCCGCGGTCCGGGCGCGC**ATG**CGGGGACCTCGCTGCTGCTG
 TCGGTTCTGCGGCCCGCAGGGGCCGCTGGCCGTGGGCATCTCCCTGGGCTTACCCCTGAGCCT
 GCTACGCGTACCTGGGTGGAGGAGCGCTGCGGCCACAGGCCGCCCAACCTGGAGACTCTG
 AGCTGCCGCGCGCGGCCAACACCAACGCGGCGCGCGGCCCAACTCGGTGACGCGCGGAGCG
 GAGCGCGAGAAGCCCGGGGCCGCGAAGGCGCGGGGAGAATTGGGAGCGCGCGCTTTGCC
 CTACCACCTGACAGCCCGGCCAGGCCGCCAAAAGGCCGTGAGACCCGCTACATCAGCA
 CGGAGCTGGGCATCAGGCAGAGGCTGCTGGTGGCGGTGCTGACCTCTCAGACACGCTGCC
 ACGCTGGGCGTGGCCGTGAACCGCACGCTGGGGCACCGGCTGGAGCGTGTGGTGTCTCTGAC
 GGGCGCAGCGGGCCGCCGGGCCCCACCTGGCATGGCAGTGGTGACGCTGGGCGAGGAGCGAC
 CCATTGGACACCTGCACCTGGCGCTGCGCCACCTGCTGGAGCAGCACGGCGACGACTTTGAC
 TGGTTCTTCTGCTGGTGCCTGACACCACTACACCGAGGCGCACGGCTGGCACGCCCTAACTGG
 CCACCTCAGCCTGGCCTCCGCCGCCACCTGTACCTGGGCGGGCCCCAGGACTTCATCGGGG
 GAGAGCCCAACCCCGCGCTACTGCCACGGAGGCTTTGGGGTGTGCTGTCTGCGCATGCTGT
 TGCACAACTCGGCCCACTGGAAGGCTGCCGCAACGACATGCTCAGTGGCGGCCCTGAC
 CGAGTGGCTGGGTGCTGCATTCTCGATGCCACCGGGTGGGCTGCACCTGGTGACACGAGG
 GGGTGCACCTATAGGCACTGAGGCTGAGCCCTGGGGAGCCAGTGCAGGAGGGGGACCTCAT
 TTCCGAAGTCCCTGACAGCCCAACCTGTGCGTGGACCTGTGCACATGTACAGCTGCACAA
 AGCTTTGCCCGAGCTGAAGCTGGAACGCACGTACACAGGAGATCCAGGAGTTACAGTGGGAGA
 TCCAGAATACAGGCATCTGCGCCTTGATGGGGACCGGGCAGCTGCTTGGCCCGTGGGTATT
 CCAGCACCATCCCGCCCGGCTCCCGCTTTGAGGTGCTGCGCTGGGACTACTTCACGAGGCA
 GCACGCTTTCTCTGCGCCGATGGCTCACCCCGCTGCCCACTGCGTGGGGCTGACCGGGCTG
 ATGTGGCCGATGTTCTGGGGACAGCTCTAGAGGAGCTGAACCGCGCTACCAACCCGGCCTTG
 CGGCTCCAGAAGCAGCAGCTGGTGAATGGCTACCGAGCCTTTGATCCCGCCGGGGTATGGA
 ATACACGCTGGACTTGCAGCTGGAGGCACCTGACCCCCAGGAGGCGCGCGGCCCTCACTC
 GCCGAGTGCAGCTGCTCCGGCCGCTGAGCCGCGTGGAGATCTTGCTGTGCCCTATGTCACT
 GAGGCCCTCAGTCTCACTGTGCTGCTGCCCTAGCTGCGGGTGAGCGTGACCTGGCCCTGG
 CTCTTTGGAGGCCCTTTGCCACTGCAGCACTGGAGCCTGGTGATGCTGCGGCAGCCCTGACCC
 TGCTGCTACTGTATGAGCCGCGCAGGCCACAGCGCTGGGCCATGCAGATGTCTTCGCACCT
 GTCAAGGCCACGCTGGCAGAGCTGGAGCGCGCTTTCCCGGTTGCCCGGGTGCCATGGCTCAG
 TGTGACAGACGCGCACCTCACCACTGCGCCTCATGGATCTACTCTCCAAGAAGCACCCGCG
 TGGACACACTGTTCTGCTGCGCGGGGCCAGACACGGTGTACGCGCTGACTTCTTGAACCCG
 TGCCGATGCATGCTCTCGGCTGGCAGGCCCTTCTTCCCATGCATTTCCAAGCCTTCCA
 CCCAGTGTGGCCCCACCAAGGGCCTGGGCCCCAGAGCTGGGCCGTGACACTGGCCGCT
 TTGATCGCCAGGCGAGCCAGCGAGGCTGCTTCAAACTCCGACTACGTGGCAGCCCGTGGG
 CGCCTGGCGGCAGCCTCAGAACAAAGAAGAGGAGCTGCTGGAGAGCCTGGATGTGTACGAGCT
 GTTCTCTCACTTCTCCAGTCTGCATGTGCTGCGGGCGGTGGAGCGCGGCTGCTGCAGCGCT
 ACCGGGCCAGAGCTGCAGCGCAGGCTCAGTGAGACCTGTACACCGCTGCCCTCCAGAGC
 GTGTTTGGGGCCTCGGCTCCCGAACCCAGCTGGCCATGTACTCTTTGAACAGGAGCAGGG
 CAACAGCAC**TGA**CCCCACCTGTCCCGCTGGGCCGTGGCATGGCCACAGCCACCCCACTT
 CTCCCCAAACACAGAGCCACCTGCCAGCCTGCTGGGCAGGGCTGGCCGTAGCCAGACCCC
 AAGCTGGCCCACTGGTCCCCCTCTGCGCTCTGTGGGTCCCCTGGGCTCTGGACAAGCACTGGG
 GGACGTGGCCCCAGGCCACCCACTTCTCATCCCAACCCAGTTTCCCTGCCCCCTGACGCT
 GCTGATTTCGGGCTGTGGCCTCCACGTATTATGCAAGTACAGTCTGCTGACGCCAGCCCTGC
 CTCTGGGCCCTGGGGCTGGGCTGTAGAAGAGTTGTTGGGGAAGGAGGAGCTGAGAGGGG
 GCATCTCCCAACTTCTCCCTTTTGGACCCCTGCCGAAGCTCCTGCTTTAATAAACCTGGCCA
 AGTGTGGAATAA

FIGURE 233

MRASLLLSVLRPAGFVAVGISLGFTLSLLSVTWVEEPCGPGPPQPGDSELPFRGNTNAARRP
NSVQPGAEREKPGAGEGAGENWEPRVLPYHPAQPGQAACKAVRTRYISTELGIRQLLVAVL
TSQTTLP TLGVAVNRTLGHRLERVVLTGARGRRAPPGMAVVTLGEERPIGHLHLALRHLL
QHGGDDFDWFFLVPDTTTYEAHGLARLTGHLSLASAAHLYLGRPQDFIGGEPTPGRYCHGGFG
VLLSRMLLQQLRPHLEGCRNDIVSARPDDEWLGRCIL DATGVGCTGDHEGVHYSHLELSPGEP
VQEGDPHFRSALT AHPVRDPVHMYQLHKAFARAE LERTYQEIQELQWEIQNTSHLAVDGDRA
AAWPVGI PAPS RPASRFEVLRWDYFTEQHAFSCADGSPRCPLRGADRADVADVLGTALEELN
RRYHPALRLQKQQLVNGYRRFDPARGMEYTL DLQLEALTPQGGRRPLTRRVQLLRPLSRVEI
LPVPYVTEASRLTVLLPLAAAERDLAPGFLEAFATAALEPGDAAAALTLLLLYEPRQAQRVA
HADVFAPVKAHVAELERRFPGARVPWLSVQTAAPSPLRLMDLLSKKHPLDTLFLLAGPDTVL
TPDFLNRCRMHAISGWQAFFPMHFQAFHPGVAPPQGPPELGRDTGRFRDQAASEACFYNS
DYVAARGRLAAASEQEEELLES LDVYELFLHFFSLHVLRAVEPALLQRYRAQTCSARLSEDL
YHRCLQSVLEGLGSRQTQLAMLLFEQEQQGNST

FIGURE 234

GCTCTGGCCGGCCCCGGCGATTGGTCACCGCCCGCTAGGGGACAGCCCTGGCCTCCTCTGAT
 TGGCAAGCGCTGGCCACCTCCCCACACCCCTTGCGAACGCTCCCTAGTGGAGAAAAGGAGT
 AGCTATTAGCCAATTTCGGCAGGGCCCGCTTTTGTAGAAGCTTGATTTCCTTTGAAGATGAAAG
 ACTAGCGGAAGCTCTGCCTCTTTCCCCAGTGGGCGAGGGAACTCGGGGCGATTGGCTGGGAA
 CTGTATCCACCCAAATGTCACCGATTTCCTCCTATGCAGGAAATGAGCAGACCCATCAATAA
 GAAATTTCTCAGCCTGGCCGAAAATGGTTGGCCCCACGAAGCCACGACAACTGGAGGCAAAG
 AGGGTTGCTCAACGCCCCGCCTCATTGAAAAACCAAATCAGATCTGGGACCTATATAGCGTG
 GCGGAGGCGGGGCGATGATTGTCGCGCTCGCACCCACTGCAGCTGCGCACAGTCGCATTTCT
 TTCCCGCCCCCTGAGACCCTGCAGCACCATCTGTC**ATG**GCGGCTGGGCTGTTTGGTTTGAGC
 GCTCGCCGCTCTTTTGGCGGCAGCGGCGACGCGAGGGCTCCCGCCGCCCGCGTCCGCTGGGA
 ATCTAGCTTCTCCAGGACTGTGGTCGCCCCGTCCGCTGTGGCGGGAAAGCGCCCCCAGAAC
 CGACCACACCGTGGCAAGAGGACCCAGAACCCGAGGACGAAAACCTGTATGAGAAGAACCCA
 GACTCCCATGGTTATGACAAGGACCCCGTTTGGACGTCTGGAACATGCAGACTGTCTTCTT
 CTTTGGCGTCTCCATCATCCTGGTCTTGGCAGCACCTTTGTGGCCTATCTGCCTGACTACA
 GGATGAAAGAGTGGTCCCGCCGCGAAGCTGAGAGGCTTGTGAAATACCGAGAGGCCAATGGC
 CTTCCTCATGGAATCCAATGCTTCGACCCAGCAAGATCCAGCTGCCAGAGGATGAG**TG**
ACCAGTTGCTAAGTGGGGCTCAAGAAGCACCGCCTCCCCACCCCTGCCTGCCATTCTGAC
 CTCTTCTCAGAGCACCTAATTAAAGGGGCTGAAAGCTGAA

235/330

FIGURE 235

MAAGLFGLSARRLLAAAATRG LPAARVRWESSFSRTVVAPS AVAGKRPEPTTPWQEDPEPE
DENLYEKNPD SHGYDKDPVLDVWNMRLVFFFGVSIILVLGSTFVAYLPDYRMKEWSRREAER
LVKYREANGLPIMESNCFDPSKIQLPEDE

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FIGURE 236

GGCGGCTGGGCTGTTTGGTTTGAGCGCTCGCCGTCCTTTGGCGGCAGCGGCGACGCGAGGGC
 TCCCGGCCGCCCGCTCCGCTGGGAATCTAGCTTCTCCAGGACTGTGGTCGCCCCGTCCGCT
 GTGGCGGAAAGCGGCCCCAGAACCGACCACACCGTGGCAAGAGGACCCAGAACCCGAGGA
 CGAAAAC TTGTATGAGAAGAACCAGACTCCCATGGTTATGACAAGGACCCGTTTTGGACG
 TCTGGAACATGCGACTTGTCTTCTTTGGCGTCTCCATCATCCTGGTCCTTGGCAGCACC
 TTTGTGGCCTATCTGCCTGACTACAGGATGAAAGAGTGGTCCCGCCGCGAAGCTGAGAGGCT
 TGTGAAATACCGAGAGGCCAATGGCCTTCCCATCATGGAATCCAAC TGCTTCGACCCAGCA
 AGATCCAG

FIGURE 237

GCGGCGGCT**ATG**CGGCTTGCTCTGCTCGTCTGTGCTCCTGGGGCCCGGCGGCTGGTGCCT
 TGCAGAACCCCCACGCGACAGCCTGCGGGAGGAACTGTGCATACCCCCGCTGCCTTCCGGGG
 ACGTAGCCCGCCACATTCCAGTTCCGACGCGCTGGGATTTCGGAGCTTCAGCGGGGAAGGAGTG
 TCCCATACAGGCTCTTTCCCAAAGCCCTGGGGCAGCTGATCTCCAAGTATTCTCTACGGGA
 GCTGCACCTGTCAATTCACACAAGGCTTTTGGAGGACCCGATACTGGGGGCCACCTTCTCTGC
 AGGCCCCATCAGGTGCAGAGCTGTGGGTCTGGTTCCAAAGACACTGTCACTGATGTGGATAAA
 TCTTGGAAGGAGCTCAGTAATGTCTCTCAGGGATCTTCTGCGCCTCTCTCAACTTCATCGA
 CTCCACCAACACAGTCACTCCCACTGCCTCCTTCAAACCCCTGGGTCTGGCCAATGACACTG
 ACCACTACTTTCTGCGCTATGCTGTGCTGCCGCGGAGGTGGTCTGCACCGAAAACCTCACC
 CCCTGGAAGAAGCTCTTGCCCTGTAGTTCCAAAGGCAGGCCCTCTCTGTGCTGCTGAAGGCAGA
 TCGCTTGTTCCACACCAGCTACCACTCCCAAGGAGTGCATATCCGCCCTGTTTGCAGAAATG
 CACGCTGTACTAGCATCTCCTGGGAGCTGAGGCAGACCCTGTCAGTTGTATTGTATGCCTTC
 ATCACGGGGCAGGGAAGAAAGACTGGTCCCTCTTCCGGATGTTCTCCCGAACCTTCACGGA
 GCCCTGCCCCCTGGCTTCAGAGAGCCGAGTCTATGTGGACATCACCACTACACACAGGACA
 ACGAGACATTAGAGGTGCACCCACCCCGACCCTACATATCAGGACGTCATCTTAGGCACT
 CGGAAGACCTATGCCATCTATGACTTGCTTGACACCGCCATGATCAACAACCTCTCGAAACCT
 CAACATCCAGCTCAAGTGAAGAGACCCCCAGAGAATGAGGCCCCCAGTGCCCTTCTCTGC
 ATGCCAGCGGTGAGTGGCTATGGGCTGCAGAAGGGGGAGCTGAGCACACTGCTGTAC
 AACACCCACCCATACCGGGCCTTCCCGGTGCTGCTGCTGGACACCGTACCCTGGTATCTGGG
 GCTGTATGTGCACACCTTCACCATCACTTCCAAAGGGCAAGGAGAACAACCAAGTTACATCC
 ACTACAGCCTGCCCAGGACCGGCTGCAACCCACCCTCTGGAGATGCTGATTCACTGCCG
 GCCAACTCAGTCACCAAGGTTTCCATCCAGTTTGAGCGGGCGCTGCTGAAGTGGACCGAGTA
 CACGCCAGATCCTAACCATGGCTTCTATGTACGCCATCTGTCTCAGCGCCCTTGTGCCCA
 GCATGTAGCAGCCAAGCCAGTGGACTGGGAAGAGAGTCCCTCTTCAACAGCCTGTTCCTCA
 GTCTCTGATGGCTCTAACTACTTTGTGCGGCTCTACACGGAGCCGCTGCTGGTGAAGCTGCC
 GACACCGGACTTCAGCATGCCCTACAACGTGATCTGCCTCACGTGCATGTGGTGGCCGTGT
 GCTACGGCTCCTTACAACTCCTCACCCGAACCTTCCACATCAGGAGCCCCGCACAGGT
 GGCCTGGCCAAGCGGCTGGCCAACCTTATCCGGCGCGCCCGAGGTGTCCCCCACT**TGA**ATT
 CTTGCCCTTTCCAGCAGCTGCAGCTGCCGTTTCTCTCTGGGAGGGGAGCCCAAGGCTGTT
 TCTGCCACTTGCTCTCCTCAGAGTTGGCTTTTGAACCAAAAGTGCCCTGGACCAAGGTGAGGGC
 CTACAGCTGTGTTTCCAGTACAGGAGCCACGCCAAATGTGGCATTGAAATTTGAATTTAA
 CTAGAAATTCATTCTCACTGTAGTGCCACCTCTATATTGAGGTTGCTCAATAAGCAAA
 AGTGGTGGGTGGCTGCTGTAATTGGACAGCACAGAAAAGATTTCATCACCACAGAAAGGTC
 GGCTGGCAGCACTGGCCAAGGTGATGGGTGTGCTACACAGTGTATGTCACTGTGTAGTGGA
 TGAGGTTTACTGTTTGTGGAATAAAAACGGCTGTTTCCGTGGAAAAA

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FIGURE 238

MPLALLVLLLLPGGWCLAEPPRDSLREELVITPLPSGDVAATFQFRTRWDSELQREGVSHY
RLFPKALGQLISKYSLRELHLSFTQGFWRTRYWGPPFLQAPSGAELWVWFQDTVTDVDKSWK
ELSNVLSGIFCASLNFIDSTNTVTPTASFKPLGLANDTDHYFLRYAVLPREVVCTENLTPWK
KLLPCSSKAGLSVLLKADRLFHTSYHSQAVHIRPVCARNACTSISWELRQTLSSVVFDAFITG
QGKKDWSLFRMFSRTLTEPCPLASESRVYVDITTYNQDNETLEVHPPPTTTYQDVILGTRKT
YAIYDLLDTAMINNSRNLNIQLKWKRPPENEAPPVPFLHAQRYVSGYGLQKGELSTLLYNTH
PYRAFPVLLLDTPWYLRLYVHTLTITSKGKENKPSYIHYQPAQDRLQPHLLEMLIQLPANS
VTKVSQIFERALLKWTEYTPDPNHGFYVSPSVLSALVPSMVAAPVDWEESPLFNSLFPVSD
GSNYFVRLYTEPLLVNLPTPDFSMPYNVICLTCTVVAVCYGSFYNLLTRTFHIEEPRTGGLA
KRLANLIRRARGVPPL

CAACATGCGGGTCCAGAGCTTCTTGGTCCTCATGGTGTCTCTCGTTCTTGTGACCTTGGTGG
CTGTGGAAGGAGTTAAAGAGGGTATAGAGAAAGCAGGGGTTTGCCACAGTGACAACTACGC
TGCTTCAAGTCCGATCTCTCCCAAGTGCACACAGACCAGGACTGTCTGGGGGAAAGGAAGT
TTGTTACCTGCACGTGTGGCTTCAAGTGTGTGATTCTCTGTGAAGGAAGTGAAGAAGGAGGAA
ACAAGGATGAAGATGTGTCAAGGCCATACCTGAGCCAGGATGGGAGGCCAAGTGTCCAGGC
TCCTCCTCTACAGGTTGTCCTCAGAAATGATGCTGGGTCTTCTCTAGCTCTGGGGGTCACTC
TCACTTGGCACCTGCCCTTGAGGGTCTGAGACTTGGAATATGGAAGAAGCAATACCCAACC
CCACCAAAGAAAACCTGAGCTTGAAGTCTTTTCCCCAAAAGAGGGAAGAGTCAAAAAAG
TCCAGACCCAGGGACGGTACTTTCCTCTCTACCTGGTGTCTCTCCTAATGCTCATGAAT
GGACCCCTCATGAATGAAACCAAGTGCCCTTATAAGAGACCCCAAAGAGCTGCCTTGCCCTTC
TGCAATGTGTGTACACAGCTAGAAGGCACGTGCAGAGAAGAGAACTGGTCTCACCAGATG
CTGAATCTGCTGTGCTGCTTGATCTTGGACTTCCAGCCTCTAGAAGTGAAGAAATAAATAT
TTGCTGTTTATAATCCAA

FIGURE 240

MGSSSFVLVMVSLVLVTLVAVEGVKEGIEKAGVCPADNVRCFKSDPPQCHTDQDCLGERKCC
YLHCGFKCVIPVKELEEGGNKDEDVSRPYPEPGWEAKCPGSSSTRCPQK

Signal sequence:

amino acids 1-19

N-myristoylation sites:

amino acids 23-29, 27-33, 32-38, 102-108

WAP-type 'four-disulfide core' domain signature:

amino acids 49-63

FIGURE 241

AAACTCAGCACTTGCCGGAGTGGCTCATTGTTAAGACAAGGGGTGTGCACTTCTTGCCAGG
 AAACCTGAGCGGTGAGACTCCCAGCTGCCTACATCAAGGCCCCAGGACATGCAGAACCTTCC
 TCTAGAACCCGACCCACCACC**ATG**AGGTCCTGCCTGTGGAGATGCAGGCACCTGAGCCAAGG
 CGTCCAGTGGTCCCTTGCTTCTGGCTGTCTGGTCTTCTTTCTTCTGCGCTTGCCCTCTTTTA
 TTAAGGAGCCTCAAAACAAAGCCTTCAGGCATCAACGCACAGAGAACATTAAAGAAAGGTCT
 CTACAGTCCCTGGCAAAGCCTTAAGTCCCAGGCACCCACAAGGGCGAGGAGGACAACCATCTA
 TGCAGAGCCAGCGCCAGAGAACAATGCCCTCAACACACAACCCAGCCCCAAGGCCACACCA
 CCGGAGACAGAGGAAAGGAGGCCAACAGGCACCGCCGGAGGAGCAGGACAAGGTGCCCCAC
 ACAGCACAGAGGGCAGCATGGAAGAGCCAGAAAAAGAGAAAACCATGGTGAACACACTGTC
 ACCCAGAGGGCAAGATGCAGGGATGGCTCTGGCAGGACAGAGGCCACAATCATGGAAGAGCC
 AGGACACAAGACACCCAAGGAAATGGGGGCCAGACCAGGAAGCTGACGGCTCCAGGACG
 GTGTCAAGAAAGCACCGAGGCCAAAGCGGCAACACAGCCAAAGACGCTCATTCACAAAAGTCA
 GCACAGAATGCTGGCTCCACAGGAGCAGTGTCAACAAGGACGAGACAGAAAGGAGTGACCA
 CAGCAGTCTATCCACCTAAGGAGAAGAAACCTCAGGGCACCCACCCCTGCCCTTTCCAG
 AGCCCCACGACGACAGAGAAACCAAAGACTGAAGGCCGCCAACTTCAAATCTGAGCCTCGGTG
 GGATTTTGAGGAAAAATACAGCTTCGAAATAGGAGGGCTTCAGAGCAGTTCGCCCTGACTCTG
 TGAAGATCAAAGCCTCAAAGTCGCTGTGGCTCCAGAACTCTTCTGCCAACCTCACTCTC
 TTCCTGGACTCCAGACACTTCAACCAGAGTGAGTGGGACCGCCTGGAACACTTGGACCAACC
 CTTTGGCTTCATGGAGCTCAACTACTCCTTGGTGAGAAAGTCTGTGACACGCTTCCCTCCAG
 TGCCCCAGCAGCAGCTGCTCCTGGCCAGCCTCCCCGCTGGGAGCCTCCGGTGATCACCTGT
 GCCGTGGTGGGCAACGGGGGCATCCTGAACAACCTCCACATGGGCGAGGATAGACAGTCA
 CGACTACGTGTTCCGATTGAGCGGAGCTCTATTAAAGGCTACGAACAGGATGTGGGGACTC
 GGACATCCTTCTACGGCTTTACCGCCTTCTCCTGACCCAGTCACTCCTTATATTGGGCAAT
 CGGGGTTTCAAGAACGTGCCCTTTGGGAAGGACGTCCGCTACTTGCATTCTCTGGAAGGCAC
 CCGGACTATGAGTGGCTGGAAGCACTGCTTATGAATCAGACGGTGATGTCAAAAACCTTT
 TCTGGTTCAGGCACAGACCCAGGAAGCTTTTTCGGGAAGCCCTGCACATGGACAGGTACCTG
 TTGCTGCACCAGACTTTCTCCGATACATGAAGAACAGGTTTCTGAGGTCTAAGACCTTGGA
 TGGTGGCCACTGGAGGATATACCGCCCCACCACTGGGGCCCTCCTGCTCACTGCCCTTC
 AGCTCTGTGACCAGGTGAGTCTTATGGCTTCATCACTGAGGGCCATGAGCGCTTTTCTGAT
 CACTACTATGATACATCATGGAAGCGGCTGATCTTTTACATAAACCATGACTTCAAGCTGGA
 GAGAGAAGTCTGGAAGCGGCTACACGATGAAGGATAAATCCGGCTGTACCAAGCTCCTGGTC
 CCGGAACCTGCCAAAGCCAAAGAACT**GGA**CGGGGCCAGGGCTGCCATGGTCTCCTTGCTGTCT
 CAGGACAGGATACAGTGGGAATCTTGAGACTCTTTGGCCACTCTTGGCCATGGCTCAGACTAA
 GCTCCAAGCCCTTCAGGAGTTCCAAGGGAACACTTGAACCATGGACAAGACTCTCTCAAGAT
 GGCAATGGCTAATTGAGGTTCTGAAGTCTTCTCAGTACATTGCTGTAGGTCTCTGAGGCCAGG
 GATTTTAAATTAATGGGGTGATGGGTGGCCAAATACCACAATCTCTGCTGAAAAACACTCTT
 CCAGTCCAAAAGCTCTTGTATACAGAAAAAGAGCCTGGATTTACAGAAACATATAGATCTG
 GTTTGAATCCAGATCAGGTTTACAGTTGTGAATCTTGAAGGTATTACTTAACTTCACTAC
 AGATTGCTAGAAGACCTTTCTAGGAGTTATCTGATTCTAGAAGGTTCTATACCTTGCTGT
 TCTTTAAGCTATTTGACAACCTCTACGTGTTGTAGAAAACCTGATAATAATACAAATGATTGT
 GTCCATGGAAAGGCCAAATAAATTTTCTACAGTGAAAAA

FIGURE 242

MRSCLWRCRHLSQGVQWSLLLAFLVFFLFALPSFIKEPQTKPSRHQRTEENIKERSLQSLAKP
 KSQAPTRARRTTIYAEPAPENNALNTQTQPKAHTTGDGRGKEANQAPPEEQDKVPHTAQRAAW
 KSPEKEKTMVNTLSPRGQDAGMASGRTEAQSWKSQDTKTTQGNNGQTRKLTASRTVSEKHQG
 KAATTAKTLIPKSQHRMLAPTGAIVSTRTRQKGVTAVIPPEKPKQATPPPAPFQSPPTQRN
 QRLKAANFKSEPRWDFEEKYSFEIGGLQTTCPDSVKIKASKSLWLQKFLPNLTLFLDSRHF
 NQSEWDRLEHFAPPFQFMELNYSLVQKVVTFRPPVPPQQLLLASLPAGSLRCITCAVVGNGG
 ILNNSHMQEIDSHDYVFRLSGALIKGYEQDVGTRTSFYGFATAFSLTQSLILGNRGFKNVP
 LGKDVRYLHFLEGTRDYEWLEALLMNQTVMSKNLFWFRHRPQEAFFREALHMDRYLLHLPDFL
 RYMKNRFLRSKTLTGAHWRIYRPTTGALLLTALQLCDQVSAYGFITEGHERFSDHYDTSW
 KRLIFYINHDFKLEREVWKRLHDEGIIRLYQRPGPGTAKAKN

Cytoplasmic Domain:

amino acids 1-10

Type II Transmembrane Domain:

amino acids 11-35

Luminal catalytic Domain:

amino acids 36-600

Ribonucleotide Reductase small subunit Signature:

amino acids 481-496

N-glycosylation Sites:

amino acids 300-303, 311-314, 331-334, 375-378, 460-463

FIGURE 243

CGATGCGCGGACCCGGGCACCCCTCCTCCTGGGGCTGCTGCTGGTGCTGGGGCCTTCGCCG
GAGCAGCGAGTGGAAATTGTTCCCTCGAGATCTGAGGATGAAGGACAAGTTTCTAAACACCT
TACAGGCCCTCTTTATTTTAGTCCAAAGTGCAGCAACACTTCCATAGACTTTATCACAACA
CCAGAGACTGCACCATTCTGCATACTATAAAAGATGCGCCAGGCTTCTTACCCGGCTGGCT
GTCAGTCCAGTGTGCATGGAGGATAAGTGAGCAGACCGTACAGGAGCAGCACACCAGGAGCC
ATGAGAAGTGCCTTGGAACCAACAGGGAAACAGAACTATCTTTATACACATCCCCTCATGG
ACAAGAGATTTATTTTGCAGACAGACTCTTCATAAGTCCTTTGAGTTTGTATGTTGTTG
ACAGTTTGCAGATATATATTCGATAAATCAGTGTACTTGACAGTGTTATCTGTCACTTATTT

244/330

FIGURE 244

MRGPGHPLLLGLLLVLGPSPEQRVEIVPRDLRMKDKFLKHLTGPLYFSPKCSKHFHRLYHNT
RDCTIPAYYKRCARLLTRLAVSPVCMDK

0991181.11601
T09TTF.TBTT660

FIGURE 245

GGGCTGGGCCCCGCCGAGCTCCAGCTGGCCGGCTTGGTCCTGCGGTCCCTTCTCTGGGAGG
 CCCGACCCCGGCCGCGCCAGCCCCACCA**ATG**CCACCCGCGGGGCTCCGCCGGGCCGCGCCG
 CTCACCGCAATCGCTCTGTTGGTGCTGGGGGCTCCCCCTGGTGCTGGCCGCGAGGACTGCCT
 GTGGTACCTGGACCGGAATGGCTCCTGGCATCCGGGGTTTAACTGCGAGTTCTTCACCTTCT
 GCTGCGGGACCTGCTACCATCGGTACTGCTGCAGGGACCTGACCTTGCTTATCACCGAGAGG
 CAGCAGAAGCACTGCCTGGCCTTCAGCCCCAAGACCATAGCAGGCATCGCCTCAGCTGTGAT
 CCTCTTTGTTGCTGTGGTTGCCACCACCATCTGCTGCTTCTCTGTTTCTGTTGCTACCTGT
 ACCGCCGGCGCCAGCAGCTCCAGAGCCCATTTGAAGGCCAGGAGATTCCAATGACAGGCATC
 CCAGTGCAGCCAGTATACCCATACCCCCAGGACCCCAAAGCTGGCCCTGCACCCCCACAGCC
 TGGCTTCATGTACCCACCTAGTGGTCCTGCTCCCCAATATCCACTCTACCCAGCTGGGCCCC
 CAGTCTACAACCCCTGCAGCTCCTCCTCCCTATATGCCACCACAGCCCTCTTACCCGGGAGCC
TGAGGGAACCGCCATGTCTCTGCTGCCCCCTTCAGTGATGCCAACCTTGGGAGATGCCTTCAT
 CCTGTACCTGCATCTGGTCCTGGGGGTGGCAGGAGTCTCCAGCCACCAGGCCCCAGACCAA
 GCCAAGCCCTGGGCCCTACTGGGGACAGAGCCCCAGGGAAGTGGAACAGGAGCTGAACTAGA
 ACTATGAGGGGTGGGGGGAGGGCTTGAATTATGGGCTATTTTTACTGGGGGCAAGGGAGG
 GAGATGACAGCCTGGGTACAGTGCCTGTTTCAAATAGTCCCTCTGCTCCCAAGATCCCAG
 CCAGGAAGGCTGGGGCCCTACTGTTGTCCCCTCTGGGCTGGGGTGGGGGGAGGGAGGAGGT
 TCCGTGAGCAGCTGGCAGTAGCCCTCCTCTCTGGCTGCCCACTGGCCACATCTCTGGCCTG
 CTAGATTAAAGCTGTAAGACAAAA

FIGURE 246

MPPAGLRRAAPLTAIALLVLGAPLVLAGEDCLWYLDNRGSHWHPGNCEFFTCCGTCYHRYC
CRDLTLLITERQQKHCLAFSPKTIAGIASAVILFVAVVATTICCFLSCCCYLRRRQQLQSP
FEGQEIPMTGIPVQVPVYPQDPKAGPAPPQPGFMYPPSGPAPQYPLYPAGPPVYNPAAPP
YMPPQPSYPGA

Transmembrane Domains:

amino acids 10-28, 85-110

N-glycosylation Site:

amino acids 38-41

N-myristoylation Sites:

amino acids 5-10, 88-93

FIGURE 247

GGGGGAGCTAGGCCGGCGGCAGTGGTGGTGGCGCGCGCAAGGGTGAGGGCGGCCCCAGAA
 CCCCAGGTAGGTAGAGCAAGAAAGATGGTGTCTGCCCTCAAATGGTCCCTTGCAACCATG
 TCATTTCTACTTTCCCTCACTGTGGCTCTCTTAAGTGTCCACTCCCTCATGGGTGCAGAG
 CACTGAAGCATCTCCAAAACGTAGTGATGGGACACCATTTCCTTGGAAATAAATACGACTTC
 CTGAGTAGCTCATCCCGATTCAATTATGATCTCTTGATCCATGCAAACTTACCACGCTGACC
 TTCTGCGGAAACCCAGAAATAGAAAATCACAGCCAGTCAGCCACACGACCATCTCTGCA
 TAGTCAGGCTGAGATATCTAGGGCCACCCCTCAGGAAGGGAGCTGGAGAGAGCTATCCG
 AAGAACCCTGCAAGTCTGGAACACCCCTCAGGAGCAAAATGCATGCTGGCTCCCGAG
 CCCCTCTTGTGGGCTCCCGTACACAGTTGTCACTCACTATGCTGGCAATCTTTCGGAGAC
 TTTCCACGGATTTTACAAAAGCACCTACAGAACCAAGGAAGGGGAAGCTGAGGATACAGCAT
 CAACACAATTTGAACCCACTGCAGCTAGAATGGCCTTCCCTGCCTTGATGAACCTGCCTTC
 AAAGCAAGTTTCTCAATCAAATTAGAAGAGAGCCAAAGGCACCTAGCCATCTCCAATATGCC
 ATTGGTGAATCTGTGACTGTTGCTGAAGGACTCATAGAAGACCATTTTGATGTCACTGTGA
 AGATAGCACCTATCTGGTGGCCTTCATCATTTAGATTTTGAAGTCTGTCAAGCAAGATAACC
 AAGAGTGGAGTCAAGGTTTCTGTTTATGCTGTGCCACAGATAAATCAAGCAGATTATGC
 ACTGGATGCTGCGGTGACTCTTCTAGAATTTTATGAGGATTTATTCAGCATACCGTATCCCC
 TACCCAAAACAAGATCTTGCTGCTATTCGACATTCGCTGCTGCTGCTATGGAAAACCTGGGGA
 CTGACACACATATAGAGATCTGCTCTGTTGTTTGATGCAGAAAAGTCTTCTGCATCAAGTAA
 GCTTGGCATCACAGTGACTGTGGCCCATGAAGTGGCCACCGAGTGGTTTGGGAACCTGGTCA
 CTATGGAATGGTGGAAATGATCTTTGGCTAAATGAAGGATTTGCCAAATTTATGGAGTTTGTG
 TCTGTCAAGTGTGACCATCTGAACTGAAAGTTGGAGATTTATCTTTGGCAAATGTTTGTGA
 CGCAATGGAGGTAGATGCTTTAAATTCCTCACACCCCTGTGTCTACACCTGTGGAAAATCTGT
 CTCAGATCCGGGAGATGTTTGATGATGTTTCTTATGATAAGGAGCTTGTATTTCTGAATATG
 CTAAGGAGTATCTAGCGCTGACGCATTTAAAGTGGTATGTGACAGTATCTCCAGAAGCA
 TAGCTATAAAAAATCAAAAAACGAGGACCTGTGGGATAGTATGGCAAGTATTTGCCCTACAG
 ATGGTGTAAAGGGATGGATGGCTTTTGCTCTAGAAGTCAACATTCATCTCATCTCACAT
 TTGCTATCAGGAAGGATGGATGTGAAAACCATGATGAACACTTGGACACTGGCAGGGGGTTT
 TCCCCTAATTAACCATCACAGTGAGGGGGAGGAATGTACACATGAAGCAAGAGCACTACATGA
 AGGGCTCTGACGGCGCCCGGACACTGGGTACCTGTGGCATGTGCCATGTGACATTCATCACCC
 AGCAAAATCCAACATGGTCCATCGATTTTGCTAAAAACAAAAACAGATGTGCTCACTCTCCC
 AGAAGAGGTGGAATGGATCAAATTTAATGTGGCATGAATGGCTATTACATTTGTGATTACG
 AGGATATGGATGGGACTCTTTGACTGGCCTTTTAAAGGAACACACAGCAGTCAAGCAGT
 AATGATCGGCAAGTCTCATTAACAAATGCATTTCAAGCTCGTCAGCATTTGGGAAGCTGTCCAT
 TGAAAAGGCTTGGATTTATCCCTGTACTTGAACATGAAGTGAATTTATGCCCTGTGTTTC
 AAGGTTTGAATGAGCTGATTCCTATGTATAAGTTAATGGAGAAAAGAGATGAATGAAGTGA
 GAACTCAATTCAGGCTTCTCTCATCAGGCTGCTAAGGGACCTCATTGATAAGCAGACATG
 GACAGACGAGGGCTCAGTCTCAGAGCAAAATGCTGCGGAGTGAACACTACTCTCTCGCTGTG
 TGCACAACTCATCAGCCGTGCCGTACAGAGGGCAGAAGGCTATTTTCAGAAAGTGGAAAGGAATCC
 AATGGAACCTTGAGCCGTGCTGTGCGAGTGTGACCTTGGCAGTGTGCTGTGGGGGCCAGAG
 CACAGAGGCTGGGATTTTCTTTATAGTAAATATCAGTTTTCTTTGTCCAGTACTGAGAAAA
 GCGAAATGAATTTGCCCTCTGCAGAACCCAAAATGAAGAAAAGCTTCAATGGCTCATAGAT
 GAAAGCTTTAAGGGAGATAAAATAAAACCTCAGGAGTTTCCACAAATCTTACACTCATTTGG
 CAGGAACCCAGTAGGATACCAACTGGCCTGGCAATTTCTGAGGAAAAACCTGGAAACAACTTG
 TACAAAAGTTGAACTTGGCTCATCTTCATAGCCACATGGTAAATGGGTACAACAAATCAA
 TTTCTCACAGAAGACAGCGCTTGAAGAGGTAAAGGATTTCTCAGCTTTTGAAGAAAAATGG
 TTTCTAGCTCCGTTGTGTCCAAACAGACAAATGAACCAATGAAGAAAAACATCGGTTGGATGG
 ATAAGAATTTGATAAAATCAGAGTGTGGCTGCAAGTGAAGCTGTGAACGTATGTAAATG
 TTCTCCCTTGGCCGGTTTCCGTGTTATCTCTAATCACCACAAATTTTGTGTGAGTGTATTTCAA
 ACTAGAGATGGCTGTTTTCCTTCCAACTGGAGATACTTTTTCCCTTCAACTCATTTTGTGA
 CTATCCCTGTGAAAAGATAGCTGTTAGTTTTCATGAATGGGCTTTTCTCATGAATTTGGGCTA
 TCGCTACCATGTGTTTGTTCATCACAGGTGTTGCCCTGCAACGTAAACCCAGAGTGTGGGT
 TCCCTGCCACAGAAGAATAAAGTACCTTATTCTTCTCAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 248

MVFLPLKWSLATMSFLLSSLLALLTVSTPSWCQSTEASPKRSDGTPFPWNKIRLPEYVIPVH
 YDLLIHANLTTLTFWGTTKVEITASQPTSTIILHSHHLQISRATLRKGAGERLSEELQVLE
 HPPQEQIALLAPEPLLVGLPYTVVIHYAGNLSETFHGFYKSTYRTKEGELRILASTQFEPTA
 ARMAFPCFDEPAFKASFSIKIRREPRHLAISNMPLVKSVTVAEGLIEDHFDVTVKMSTYLVA
 FIISDFESVSKITKSGVKVSVYAVDPKINQADYALDAAVTLLEFYEDYFSIPYPLPKQDLAA
 IPDFQSGAMENWGLTTYRESALLFDAEKSSASSKLGITVTVAHELAHQWFGNLVTMEWWNDL
 WLNIEGFAKFMEFVSVSVTHPELKVGDYFFGKCFDAMEVDALNSSHPVSTPVENPAQIREMFD
 DVSYDKGACILNMLREYLSADAFKSGIVQYLQKHSYKNTKNEDLWDSMASICPTDGVKGMDS
 FCSRSQHSSSSSHWHQEGVDVKTMMNTWTLQRGFPLITITVRGRNVHMKQEHYMKGSDGAPD
 TGYLWHVPLTFITSKSNMVHRELLKTKTDVLILPEEVEWIKFNVGMNGYYIVHYEDDGWDSL
 TGLLKGTHTAVSSNDRASLINNAFQLVSIKLSIEKALDLSLYLKHETEIMPVQGLNELIP
 MYKLMKMRDMNEVETQFKAFLIRLLRDLDKQWTWDEGSVSEQMLRSELLLLACVHNYQPCV
 QRAEYFRKWKESNGNLSLPVDVTLAVFAVGAQSTEGWDFLYSKYQFSLSTEKSQIEFALC
 RTQNKEKLQWLDESFKGDKIKTQEFPQILTIGRNPVGYPLAWQFLRKNWNKLQKFEELGS
 SSIAHMVMGTNTQFSTRLEEVKGFFSSLKENGSQLRCVQQTITETIENIGWMDKNFDKIR
 VWLQSEKLERM

Signal peptide:

amino acids 1-34

N-glycosylation sites:

amino acids 70-74, 154-158, 414-418, 760-764, 901-905

Neutral zinc metalloproteases, zinc-binding region signature:

amino acids 350-360

FIGURE 249

CAGCCACAGACGGGTC**ATG**AGCGCGGTATTACTGCTGCCCTCCTGGGGTTTACCTCCCAC
 TGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTTCAGCATGTGTGGAAGGTGTCC
 GACCTACCCCGCAATGGACCCCTAAGAACACCACTGCGACAGCGGCTTGGGGTGCCAGGA
 CACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGTCTCCAAGGGCTGCACGG
 AGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCTCTCCCTGATC
 TCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAACTCCCTCCCCTG
 TTGGGCCCCACAGCCCCAGCAGACCCAGGATCCTTGAGGTGCCAGTCTGCTTGTCTATGG
 AAGGTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGACCACACTGTTATGAT
 GGCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCC
 CCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTTGGGCCCGTGGGTATGACTGAGA
 ACTGCAATAGGAAAGATTTTCTGACCTGTCTCGGGGACCACCATTATGACACACGGAAAC
 TTGGCTCAAGAACCCTGATGATGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGT
 GTGTGAGGAGACGCTGCTGCTCATAGATGTAGGACTCACATCAACCTCGTGGGGACAAAAG
 GCTGCAGCACTGTTGGGGCTCAAAATTCACAGAAGACCACCATCCACTCAGCCCCCTCTGGG
 GTGCTTGTGGCCTCCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAG
 CAGCGTTCTGCTGAACTCCCTCCCTCCTCAAGCTGCCCTGTCCAGGAGACCGGCAGTGTCT
 CTACCTGTGTGCAGCCCCCTTGAACCTGTTCAAGTGGCTCCCCCGAATGACCTGCCCCAGG
 GGCGCCACTCATTGTTATGATGGGTACATTATCTCTCAGGAGGTGGGCTGTCCACCAAAAT
 GAGCATTGAGGGCTGCGTGGCCCAACCTTCCAGCTTCTTGTGAACCACACAGACAAATCG
 GGATCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGT
 GGGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTG
 GTGGGGAGTGGTTTGCCCTTCTCTGCT**TAA**CTCTATTACCCCCACGATTCTTACCGCTGCTGA
 CCACCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTGGACACCGAGATTCTTTC
 CCATTCTGTCCATGAATCATCTTCCACACACAATCATTATCTACTCACCTAACAGCA
 ACACTGGGGAGAGCCTGGAGCATCGGACTTGCCCTATGGGAGAGGGACGCTGGAGGAGTG
 GCTGCATGTATCTGATAATACAGACCCTGTCTTTCA

FIGURE 250

MSAVLLLALLGFIPLPGVQALLCQFGTVQHVKVSDLPRQWTPKNTSCDSGLGCQDTLMLI
ESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPLSLISYTFVCRQEDFCNNLVNSLPLWAPQP
PADPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRRLRGGGIFSNLRVQGCMPQPGCN
LLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSENTEMCEVGQVCQETL
LLIDVGLTSTLVGKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCSASSSSVLLN
SLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSGGGLSTKMSIQGC
VAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESLTWGVGLALAPALWWGVVC
PSC

CGCAGCGGGCAGGACGCCCCGTTTCGCCCTAGCGCGTGTCTCAGGAGTTGGTGTCTCGCTCGCCT
CAGC**ATG**AGGGGGAATCTGGCCCTGGTGGGCGTTCTAATCAGCCTGGCCTTCTGTCTACTGCTG
CCATCTGGACATCTCTAGCCGGCTGGCGATGACGCCCTGCTCTGTGCAGATCCTCGTCCCTGG
CCTCAAAGGGGATGCGGGAGAGAAGGGAGACAAAGGC GCCCCGGACGGCCTGGAAGAGTCTG
GCCCCACGGGAGAAAAAGGAGACATGGGGGACAAAGGACAGAAAGGCAGTGTGGGTGCTCAT
GGAAAAATTGGTCCCATTGGCTCTAAAGGTGAGAAAGGAGATTCCGGTGACATAGGACCCCT
TGGTCTTAATGGAGAACCAAGGCTCCCATGTGAGTGCAGCCAGCTGCGCAAGGCCATCGGGG
AGATGGACAACCAAGTCTCTCAGCTGACCAGCGAGCTCAAGTTCATCAAGAATGCTGTGCGC
GGTGTGCGCGAGACGGAGAGCAAGATCTACCTGCTGGTGAAGGAGGAGAAGCGCTACGCGGA
CGCCAGCTGTCTGCCAGGGCCGCGGGGGCACGCTGAGCATGCCCAAGGACGAGGCTGCCA
ATGGCCTGATGGCCGCATACCTGGCGCAAGCCGGCTGGCCCGTGTCTTCATCGGCATCAAC
GACCTGGAGAAGGAGGGCGCCTTCGTGTACTCTGACCACTCCCCATGCGGACCTTCAACAA
GTGGCGCAGCGGTGAGCCCAACAATGCCTACGACGAGGAGGACTGCGTGGAGATGGTGGCCT
CGGGCGGCTGGAACGACGTGGCCTGCCACACCACCATGTACTTCATGTGTGAGATTGACAA
GAGAACATG**TGA**GCCTCAGGCTGGGGCTGCCATTGGGGGCCCAATGTCCTCTGAGGGTT
GGCAGGGACAGAGCCAGACCATGGTGCACAGGAGAGTGTCCCTCTGTGAAGGGTGGAG
GCTCACTGAGTAGAGGGCTTGTGTCTTAACCTAGAAAGATGGCCATGCTTAAAGAGGAAAAATG
AAAGTGTTCTCGGGGTGCTGTCTCTGAAGAAGCAGAGTTTCATTACCTGTATTGTAGCCCCA
ATGTCTATTATGTAATTATTACCCAGAATTGCTCTCCATAAAGCTTGTGCCTTTGTCCAAGC
TATACAATAAAATCTTTAAGTAGTGCAGTAGTTAAGTCCAAAAAAAAAAAAAAAAAAAAA

FIGURE 252

MRGNLALVGVLISLAFLLPSGHPQPAGDDACSVQILVPGLKGDAGEKGDKGAPGRPGRVG
PTGEKGDMDKGQKGSVGRHGKIGPIGSKGEKGDSDIGPPGPNGEPGLPCECSQLRKAIGE
MDNQVSQLTSELKFIKNAVAGVRETESKIYLLVKEEKRYADAQLSCQGRGGTLSMPKDEAAN
GLMAAYLAQAGLARVFIGINDLEKEGAFVYSDHSPMRTFNKWRSGEPNNAYDEEDCVEMVAS
GGWNDVACHTTMYFMCEFDKENM

099131.11601

FIGURE 253

AGTGACTGCAGCCTTCCTAGATCCCCTCCACTCGGTTTCTCTCTTTGCAGGAGCACCGGCAG
 CACCAGTGTGTGAGGGGAGCAGGCAGCGGTCTTAGCCAGTTCCTTGATCCTGCCAGACCACC
 CAGCCCCCGGCACAGAGCTGCTCCACAGGCACCATGAGGATCATGCTGCTATTACAGCCAT
 CCTGGCCTTCAGCCTAGCTCAGAGCTTTGGGGCTGTCTGTAAGGAGCCACAGGAGGAGGTGG
 TTCCTGGCGGGGGCCGAGCAAGAGGGATCCAGATCTCTACCAGCTGCTCCAGAGACTCTTC
 AAAAGCCACTCATCTCTGGAGGGATTGCTCAAAGCCCTGAGCCAGGCTAGCACAGATCCTAA
 GGAATCAACATCTCCCAGAAAACGTGACATGCATGACTTCTTTGTGGGACTTATGGGCAAGA
 GGAGCGTCCAGCCAGAGGAAAGACAGGACCTTTCTTACCTTCAGTGAGGGTTCTCGGCCC
 CTTTCATCCCAATCAGCTTGGATCCACAGGAAAGTCTTCCCTGGGAACAGAGGAGCAGAGACC
 TTTATTAAGACTCTCCTACGGATGTGAATCAAGAGAAGTCCCCAGCTTTGGCATCCTCAAGT
 ATCCCCCGAGAGCAGAATAGGTACTCCACTTCCGGACTCCTGGACTGCATTAGGAAGACCTC
 TTTCCCTGTCCCAATCCCAGGTGCGCACGCTCCTGTTACCTTTCTCTTCCCTGTTCTTGT
 AACATTCTTGTGCTTTGACTCCTTCTCCATCTTTTCTACCTGACCCTGGTGTGAAACTGCA
 TAGTGAATATCCCCAACCCCAATGGGCATTGACTGTAGAATACCCTAGAGTTCCTGTAGTGT
 CCTACATTAAAAATATAATGTCTCTCTATTCTCAACAATAAAGGATTTTTCATATGAA
 AA

FIGURE 254

MRIMLLFTAILAFSLAQSFSGAVCKEPQEEVVPGGGRSKRDPDLYQLLQRLFKSHSSLEGLLK
ALSQASTDPKESTSPKSRDMHDFVGLMGKRSVQPEGKTGPFPLPSVRVPRPLHPNQLGSTGK
SSLGTEEQRPL

Important features:

Signal peptide:

amino acids 1-18

Tyrosine kinase phosphorylation site.

amino acids 36-45

N-myristoylation site.

amino acids 33-39, 59-65

Amidation site.

amino acids 90-94

Leucine zipper pattern.

amino acids 43-65

Tachykinin family signature.

amino acids 86-92

FIGURE 255

GGGCGTCTCCGGTCTCTCTATTGAGCTGTCTGCTCGCTGTGCCCGCTGTGCCTGCTGTGCC
 CGCGCTGTGCGCGCTGTACCGCTCTGCTGGACGCGGGAGACGCCAGCGAGCTGGTGATTG
 GAGCCCTGCGGAGAGCTCAAGCGCCAGCTCTGCCCCAGGAGCCAGGCTGCCCGTGAGTCTC
 CATAGTTGCTGCAGGAGTGAGGCCATGAGCTGCGTCCTGGTGGTGTGCATCCCCTTGGGGC
 TGCTGTTCTGGTCTGCGGATCCCAAGGTACCTCCTGCCAACGTCACTCTCTTAGAGGAG
 CTGCTCAGCAAATACCAGCACACGAGTCTCACTCCCGGGTCCGCAGAGCCATCCCCAGGGA
 GGACAAGGAGGAGATCCTCATGCTGCACAACAGCTTCGGGGCCAGGTGCAGCCTCAGGCCT
 CCAACATGGAGTACATGGTGAGCGCCGGCTCCGGCCGAGAGGCTGGCACCAGGGGTGGGGC
 CTGGGCCACCAGCCTGCTCTGTTCCCGAGCCAGCTCTGTTCCCGAGCCAGTGCCTGTGATGG
 CTGGCTCAGGCTCTCCTCTGGCAGGGGAGGATCCCGGCTCTGTTCTGTTTGTGTTGTTGTT
 TTGAGACAGGCTCACTCTGCCACTGACGCTGGAGTGCAATGGCACAATCGTCATGCCCTG
 AAACCTTAGACTCCCGGGGTTAAGCGATCCTGCTTCAGCCTCCCAAGTAGCTGGAACACAG
 GCATGCACCATGGTGCCAGCTAGATTTTAAATATTTTGTGGAGATGGGGTCTTGCTACGT
 TGCCCAGGCTGGTCTTGAACCTCTAGGCTCAAGCAATCCTCCTGCCTCAGCCTCTCAAAGTG
 CTAGGATTATAGGCATGAGTCACCTGTCTGGCTCTGGCTCTGTTCTTAACATTCTGCCAAA
 ACAACACACGTGGGTTCCCTGTGCAGAGCCTGCCTCGTTGCCTTCATGTCACTCTTGGTAGC
 TCCACTGGGAACACAGCTCTCAGCCTTTCCACCTGGAGGCAGAGTGGGAGGGGGCCAGGG
 CTGGGCTTTGCTGATGCTGATCTCAGCTGTGCCACACGCTAGCTGCACCAACCTGACTTCTC
 CTTAGCCCGTGTGAGCCTCACTTTCCACTTGGAGAGTCCTTCTCGCGTGGTTGCCATGACT
 GTGAGATAAGTCGAGGCTGTGAAGGGCCCGGCACAGACTGACCTGCCTCCCCAACCCCTAGG
 CTTTGCTAACCAGGAAAGAGCTAACGGTGACAGAAGACAGCAAGGTCAACCTCCCGGGT
 GATTGTGATGGGTGTTCCAGGTGTGGTTGGGCGATGCTGCTACTTGACCCCAAGCTCCAGTG
 TGAAACTTCCTTCTGGCTGGTTTTCCAGAACTACAGAGGAATGGACCACAGTCTTCCAGG
 GTCCCTCCTCGTCCACCAACCGGAGCCTCCACCTTGCCATCCGTCACTATGAATGGCTT
 TTTAAACAAACCCACGTCCAGCCTGGGTAAACATGGTAAAGCCCGTCTCTACAAAAAATC
 CAAGTTAGCCGGGCATGGTGGTGCACCTGTAGTCCAGCTGCAGTGGGACTGAGGTGGAG
 GTGGAGGTGGGGGTGGGAGCTGAGGAAGGAGGATCGCTTGAGCCTGGGAAGTCGAGGCTGC
 AGTGAGCTGAGATTGCACCACTGCACTCCAGCCTGGGTGACAGAGCAAGACCTGTCTCAAAA

FIGURE 256

MSCVLGGV IPLGLLFLVCGSQGYLLPNVTLLLELLSKYQHNEHSRVRRAIPREDKEEILML
HNKLRGQVQPQASNMEYMVSAAGSGRRGWHRGWGLGHQPALFPSQLCSPASACDGLRVSSGR
GGSRLCSVLFVCFETGSHSATDAGVQWHNRHALKP

Important features:**Signal peptide:**

amino acids 1-22

N-glycosylation site.

amino acids 27-31, 41-45

N-myristoylation site.

amino acids 126-132, 140-146

Amidation site.

amino acids 85-89

AAGGAGAGGCCACCGGACTTTCAGTGTCTCTCCATCCCAGGAGCGCAGTGGCCACT**ATG**GG
GTCTGGGCTGCCCTTGTCTCTCTTGACCCTCCTTGGCAGCTCACATGGAACAGGGCCGG
GTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCTATGAGTCCAGC
TTCTTGAAATTGCTTGAAAAGCTCTGCCTCCTCTCCATCTCCCTTCAGGGACCAGCGTCAC
CCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACA**TGA**CAGCCATTGAAGCTG
TGTCCTTCTTGCGCCGGGCTTTTGGCGCGGGATGCAGGAGGCAGGCCCCGACCTGTCTTT
CAGCAGGCCCCCCACCCTCCTGAGTGGCAATAAATAAAATTGGTATGCTG

258/330

FIGURE 258

MSGGLPLVLLLTLLGSSHGTGPGMTLQLKLKESFLTNSSESSFLELLEKLCLLLHLPSTGTS
VTLHHARSQHHVCNT

099101-11601

FIGURE 259

AATTGTATCTGTGTAATGTTAAAACAAACGAAATAAAATAGAAGGAAAACTTTCTGAGTTT
CAAAAACAACAGACTAGTACTCTAAAGAACTCTTTAAAAACAATTAACTGTTAGGATTGCAGT
TATGATTGGATATTATTTAATCTGTTTCTGATGTGGGGTTCCTCCACTGTGTTCTGTGTGC
TATTAATATTTACCATTGCAGAAGCTTCATTTCAGTGTGAAAATGAATGCTTAGTGGATCTG
TGCCCTTTACGCATATGTTACAAATTATCTGGAGTTCCTAATCAATGCAGAGTCCCTCCC
CTCCGATTGTTCTAAAT**TAA**TTGAAAGATGTCTGCTGTGAAAAAGGCATGTATTTAAATCTG
TATGATTCTCAACCATCTTTAGTTGGGAAAGGTCCTTGAAAGCCAATGGAAATACTTTTTTT
TTTTCTTGGCACTAATCAAGTGAGTGTTACCTTTTCACTTAGTAGGATGTGTTGTTACGCTA
GTAAATAGAAACCTGTGTTTATTCTCAGGTATTTTAGAAACAACAGCCATCATTTTATTTT
ATGTGTGTGTTCTTGGCTGTATTCTATAAATTATATATTTTGGGCTATCAAATATTACTTCAT
TCAATATAAATAACAATAGTAGAAGTTGTTTACTTAGATATGCTTCTAGTTGCATTTTCTC
AGCCTATGTAAGACTACTTTGTTGTAATAGCCTTTGAAATTTACAGTACTGTCTCTCTACTA
TCTTCAGATTACTTGATTCAATAAACCAATTATGTTTGTAATTGATTAATAAAACCAGA
ATAAAAGTTCATATCTACCC

260/330

FIGURE 260

MIGYYLILFLMWGSSTVFCVLLIFTIAEASFVENECLVDLCLLRICYKLSGVPNQCRVPLP

SDCSK

Important features:

Signal peptide:

amino acids 1-29

109777-187166

FIGURE 261

GAGGATTTTGCCACAGCAGCGGATAGAGCAGGAGAGCACCACCGGAGCCCTTGAGACATCCTT
 GAGAAGAGCCACAGCATAAGAGACTGCCCTGCTTGGTGTCTTTCAGGAGATGGTGGCCCTT
 CGAGGAGCTTCTGCATTGCTGGTTCGTCTCCTTGCAGCTTTTTCTGCCCCCGCCAGTGATC
 CCAGGACCCAGCCATGGTGCATTACATCTACCAGCGCTTTCAGATCTTGAGACCAAGGCTGG
 AAAAAATGTACCCAAAGCAACGAGGGCATACATTCAAGAATCCAAGAGTTCTCAAAAAATATA
 TCTGTCACTGCTGGGAAGATGTCAGACCTACACAAGTGAGTACAAGAGTGCAGTGGGTAACTT
 GGCACGTGAGAGTTGAACGTGCCAACGGGAGATTGACTACATACAACTCCTCGAGAGGCTG
 ACGAGTGCATCGTATCAGAGGACAAGACACTGGCAGAAATGTGCTCCAAGAAGCTGAAGAA
 GAGAAAAAGATCCGGACTCTGCTGAATGCAAGCTGTGACAACATGCTGATGGGCATAAAGTC
 TTTGAAAATAGTGAAGAAGATGATGGACACACATGGCTCTTGGATGAAAGATGCTGTCTATA
 ACTCTCCAAAGGTGACTTTATAATTGGATCCAGAAACAACACTGTTTGGGAATTTGCAAAAC
 ATACGGGCATTCATGGAGGATAACACCAAGCCAGCTCCCCGGAAGCAAACTCTAACACTTTT
 CTGGCAGGGAACAGGCCAAGTGATCTACAAAGTTTTCTATTTTTTCATAACCAAGCAACTT
 CTAATGAGATAATCAAAATATAACCTGCAGAAAGAGGACTGTGGAAGATCGAATGCTGCTCCCA
 GGAGGGGTAGGCCGAGCATTTGGTTTACCAGCACTCCCCCTCAACTTACATTGACCTGGCTGT
 GGATGAGCATGGGCTCTGGGCCATCCACTCTGGGCCAGGCCATAGCCATTGGTTCCTCA
 CAAAGATTGAGCCCGGGCACACTGGGAGTGGAGCATTATGGGATACCCCATGCAAGCCAG
 GATGCTGAAGCCCTCATTCTCTTGTGTGGGTTCTCTATGTGGTCTACAGTACTGGGGGCCA
 GGGCCCTCATCGCATCACTGCATCTATGATCCACTGGGCACTATCACTGAGGAGGACTTGC
 CCAACTTTGTTCTTCCCCAAGACCAAGAAGTCACTCCATTAACCCAGAGAT
 AAGCAGCTCTATGCTTGAATGAAGGAAACAGATCATTTACAAACTCCAGACAAAGAGAAA
 GCTGCTCTGTGAAGTAATGCATTACAGCTGTGAGAAAGAGCACTGTGGCTTTGGCAGCTGTTT
 TACAGGACAGTGAGGCTATAGCCCCCTTCAAAATATAGTATCCCTCTAATCACACACAGGAAG
 AGTGTGTAGAAGTGGAATACGTATGCCTCCTTTCCCAAATGTCACTGCCTTAGGTATCTTC
 CAAGAGCTTAGATGAGAGCATATCATCAGGAAAGTTTCAACAATGTCCATTACTCCCCAAA
 CCTCCTGGCTCTCAAGGATGACCACATTCTGATACAGCCTACTTCAAGCCTTTTGTTTACT
 GCTCCCCAGCAATTTACTGTAACCTCGCCATCTTCCCTCCCAATTAGAGTTGTATGCCAGC
 CCTAATATTACCACCTGGCTTTTCTCTCCCTGGCCTTTGCTGAAGCTCTTCCCTCTTTT
 CAAATGTCTATTGATATTCTCCCATTTTCACTGCCCACTAAAATACTATTAATATTCTTT
 CTTTTCTTTTTTTTTTTTGGAGACAAGGTCTCACTATGTGCCAGGCTGGTCTCAAACTCC
 AGAGCTCAAGAGATCCTCTGCCTCAGCCTCCTAAGTACCTGGGATTACAGGCATGTGCCAC
 CACACCTGGCTTAAATATACTATTCTTATTGAGGTTTAACTCTATTTCCCTAGCCCTGTG
 CTTTCACTAAGCTTGGTAGATGTAATAATAAAGTGAAAAATTAACATTTGAATATCGCTTT
 CCAGGTGTGGAGTGTTCACATCATTTGAATTTCTGTTTCACTTTTGTGAACATGCACAAG
 TCTTTACAGCTGTCACTTAGAGTTTAGGTGAGTAACACAATTAACAAGTGAAAGATACAGC
 TAGAAAAATCTACAAATCCCATAGTTTTTTCCATTGCCAAGGAGCATCAAAATACGTATGT
 TGTTCACCTACTCTTATAGTCAATGCGTTTATCGTTTTCAGCCTAAAAATATAGTCTGTCC
 TTTAGCCAGTTTTTCATGCTGTGCACAAGACCTTTCAATAGGCCCTTTCAAATGATTAATTCCTCC
 AGAAAACCAAGTCTAAGGGTGAGGACCCCACTCTAGCCTCCTCTTGTCTTGTCTGCTCTGT
 TTCTCTCTTTCTGCTTTAAATTCAATAAAAGTGACACTGAGCAAAAAAAAAAAAAA

0001191.111601

MMVALRGASALLVFLAFLPPQCTQDPAMVHYIYQRFVLEQGLEKCTQATRAYIQEFQE
FSKNISVMLGRCTYTSEYKSAVGNLALRVERAQRIDYIQYLREADECIVSEDKTLAEMLL
QEAEEEKKIRTLNLASCDNMLGIKSLKIVKKMMDTHGSWMKDAVNSPKVYLLIGSRNNTV
WEFANIRAFMEDNTKPA PRKQILTLWSQGTGQVIYKGLFFHNQATSNEIIKYNLQKRTVED
RMLLPGGVGRALVYQHSPSTYIDLAVDEHGLWAIHSGPGTHSHLVLTKEIPGTLGVEHSWDT
PCRSQDAEASFLLCGVLVYVYSTGGQGPHRITCIYDPLGTISEEDLPNLFPPKRPRSHSMIH
YNPRDKOLYAWNEGNOIIYKLTQKRKLPLK

FIGURE 263

GGGGCCCCGCTACTCACTAGCTGAGGTGGCAGTGGTTCCACCAAC**ATG**GAGCTCTCGCAGA
 TGTGCGAGCTCATGGGGCTGTCGGTGTGCTTGGGCTGCTGGCCCTGATGGCGACGGCGGCG
 GTAGCGCGGGGGTGGCTGCGCGCGGGGGAGGAGAGGAGCGGCGCGGCCCTGCCAAAAAGC
 AAATGGATTTCACCTGACAAATCTTCGGGATCCAAGAAGCAGAAACAATATCAGCGGATT
 GGAAGGAGAAGCCTCAACAACACAACCTTCAACCACCGCCTCCTGGCTGCGAGCTCTGAAGAGC
 CACAGCGGGAACATATCTTGCATGGACTTTAGCAGCAATGGCAAAATACCTGGCTACCTGTGC
 AGATGATCGCACCATCCGCATCTGGAGCACCAAGGACTTCCTGCAGCGAGAGCACCGCAGCA
 TGAGAGCCAACTGGAGCTGGACCACGCCACCTGGTGGCTTACAGCCCTGACTGCAGAGCC
 TTCATCGCTGGCTGGCCAAACGGGGACACCTCCGTGTCTTCAAGATGACCAAGCGGGAGGA
 TGGGGGCTACACCTTACAGCCACCCAGAGGACTTCCCTAAAAAGCACAAGGCGCCTGTCA
 TCGACATTGGCATTGCTAACACAGGGAAGTTTATCATGACTGCCTCCAGTGACACCACTGTC
 CTCATCTGGAGCCTGAAGGGTCAAGTGTCTTACCATCAACACCAACCAGATGAACAACAC
 ACACGCTGCTGTATCTCCCTGTGGCAGATTTGTAGCCTCGTGTGGCTTACCCCAAGATGTGA
 AGGTTTGGGAAGTCTGCTTTGGAAAGAAGGGGAGTTCAGGAGGTGGTGGCGAGCCTCGAA
 CTAAAGGGCCACTCCGCGGCTGTGCACTCGTTTGTCTTCCAAAGACTCACGGAGGATGGC
 TTCTGTCTCCAAGGATGGTACATGGAACACTGTGGGACACAGATGTGGAATACAAGAAGAGC
 AGGACCCCTACTTGTCTGAAGACAGGCGCTTTGAAGAGGCGGGGTGCCGCGCCTGTGCCG
 CTGGCCCTCTCCCCAACGCCAGGTCTTGGCCTTGGCCAGTGGCAGTAGTATTCATCTCTA
 CAATACCCGGCGGGGCGAGAAGGAGGAGTGTCTTGGAGCGGGTCCATGGCGAGTGTATCGCCA
 ACTTGTCTCTTGACATCACTGGCCGCTTTCTGGCCTCCTGTGGGACCGGGCGGTGCGGCTG
 TTTCACAACACTCCTGGCCACCGAGCCATGGTGGAGGAGATGCAGGGCCACCTGAAGCGGGC
 CTCCAACGAGAGCACCCGCCAGAGGCTGCAGCAGCAGCTGACCCAGGCCCAAGAGACCTGA
 AGAGCCTGGTGCCCTGAAGAAG**TGA**CTCTGGGAGGGCCCGGCGCAGAGGATTGAGGAGGAG
 GGATCTGGCCCTCCTCATGGCACTGCTGCCATCTTTCTCCAGGTGGAAGCCTTTTCAGAAGG
 AGTCTCCTGGTTTTCTTACTGTTGGCCCTGCTTCTTCCATTGAACACTACTCTTGTCTACTT
 AGGTCTCTCTCTTCTTGTGCTGTGACTCCTCCCTGACTAGTGGCCAAGGTGCTTTTCTCTC
 CTCCAGGCCCAGTGGGTGGAATCTGTCCCCACCTGGCACTGAGGAGAATGGTAGAGGGAG
 AGGAGAGAGAGAGAAATGTGATTTTGGCCTTGTGGCAGCACATCCTCACACCCAAAGAAG
 TTTGTAAATGTTCCAGAACAACCTAGAGAACACCTGAGTACTAAGCAGAGTTTGTGAAGGA
 TGGGAGACTGGGATAGCTTCCATCAAGAAGCTGTGTTCCATCAAAAAGACACTAAGGGATT
 TCCTTCTGGGCCCTCAGTTCTATTTGTAAGATGGAGAATAATCCTCTCTGTGAACCTCCTTGCA
 AAGATGATATGAGGCTAAGAGAATATCAAGTCCCCAGGTCTGGAAGAAAAGTAGAAAAGAGT
 AGTACTATTGTCCAAATGTCATAAGTGGTAAAGTGGGAACCAAGTGTGCTTTGAAACCAA
 TTAGAAACACATTCTTGGGAAGGCAAGTTTCTGGGACTTGATCATACATTTTATATGGT
 TGGGACTTCTCTCTGGGAGATGATATCTTGTTTAAAGGAGACCTCTTTTCAGTTCATCAAG
 TTCATCAGATATTGAGTGCCCACTCTGTGCCCAAATAAATATGAGCTGGGGATTAATAAAAA
 AA

FIGURE 264

MELSQMSELMGLSVLLGLLALMATAAVARGWLRAGEERSGRPACQKANGFPDPKSSGSKKQK
QYQIRIRKEKPQQHNFTHRLAAALKSHSGNISCMDFSSNGKYLATCADDRTIRIWSTKDFLQ
REHRSMRANVELDHATLVRFS PDCRAFI VWLANGDTLRVFKMTKREDGGYTFTATPEDFPKK
HKAPVIDIGIANTGKFIMTASSD TTVLIWSLKGQVLSTINTNQMNTHAAVSPCGRFVASCG
FTPDVKVWEVCFGKKGEFQEVVRAFELKGHSAAVHSFAFSNDSRRMASVSKDGTWKLWDTDV
EYKKKQDPYLLKTGRFEEAAGAAPCRLALSPNAQVLALASGSSIHLYNTRRGEKEECFERVH
GECIANLSFDITGRFLASCGDRAVRLFHNTPGHRAMVEEMQGHLKRASNESTRQLQQQLTQ
AQETLKSLGALKK

Important features:**Signal peptide:**

amino acids 1-25

N-glycosylation site.

amino acids 76-80, 92-96, 231-235, 289-293, 378-382, 421-425

Beta-transducin family Trp-Asp repeat protein.

amino acids 30-47, 105-118, 107-119, 203-216, 205-217, 296-308

FIGURE 265

TGGCCTCCCCAGCTTGCCAGGCACAAGGCTGAGCGGGAGGAAGCGAGAGGCATCTAAGCAGG
 CAGTGTTTTGCCCTTACCCCCAAGTGACCATGAGAGGTGCCACGCGAGTCTCAATCATGCTCC
 TCCTAGTAACCTGTGCTGACTGTGCTGATCACAGGGGCTGTGAGCGGGATGTCCAGTGT
 GGGGCAGGCACCTGCTGTGCCATCAGCCTGTGGCTTCGAGGGCTGCGGATGTGACCCCCGCT
 GGGGCGGGAAGGCGAGGAGTGCCACCCCGGCAGCCACAAGGTCCCTTCTTCAGGAAACGCA
 AGCACCACACCTGTCTTGCTTGCCCAACCTGCTGTGCTCCAGGTTCCCGGACGGCAGGTAC
 CGCTGCTCCATGGACTTGAAGAACATCAATTTTAGGCGCTTGCTGGTCTCAGGATACCCA
 CCATCCTTTTCTGAGCACAGCCTGGATTTTTATTCTGCCATGAAACCCAGCTCCCATGAC
 TCTCCAGTCCCTACACTGACTACCTGATCTCTTGTCTAGTACGCACATATGCACACAG
 GCAGACATACCTCCCATCATGACATGGTCCCCAGGCTGGCTGAGGATGTACAGCTTGAGG
 CTGTGGTGTGAAAGGTGGCCAGCCTGTTCTCTCCCTGCTCAGGCTGCCAGAGAGGTGGTA
 AATGGCAGAAAGGACATTCCCCCTCCCCAGGTGACCTGCTCTCTTCTGGGCCCTG
 CCCCTCTCCCCACATGTATCCCTCGGTCTGAATTAGACATTCCTGGGCACAGGCTCTTGGGT
 GCATTGCTCAGAGTCCCAGGTCTGGCTGACCTCAGGCCCTTACGTGAGGTCTGTGAGG
 ACCAATTGTGGGTAGTTCATCTTCCTCGATTGGTTAACTCCTTAGTTTCAGACCACAGAC
 TCAAGATTGGCTCTTCCAGAGGGCAGCAGACAGTCACCCAAGGCAGGTGTAGGGAGCCCA
 GGGAGGCCAATCAGCCCCCTGAAGACTCTGGTCCAGTCAGCCTGTGGCTTGTGGCCTGTGA
 CCTGTGACCTTCTGCCAGAATTGTCATGCCTCTGAGGCCCTCTTACCACACTTTACCAT
 TAACCACTGAAGCCCCCAATTCCCACAGCTTTTCCATTAAATGCAATGGTGGTGGTTCAA
 TCTAATCTGATATTGACATATTAGAAGGCAATTAGGGTGTTCCTTAAACAACCTCTTCCA
 AGGATCAGCCCTGAGAGCAGGTGGTGACTTTGAGGAGGGCAGTCTCTGTCCAGATTGGGG
 TGGGAGCAAGGGACAGGGAGCAGGGCAGGGGCTGAAAGGGGCACTGATTACAGACCAGGGAGG
 CAACTACACACCAACATGCTGGCTTTAGAATAAAAGCACCAACTGAAAAAA

FIGURE 266

MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGECHP
GSHKVPFFRKRKHHTCPCLPNLLCSRFPDGRYRCSMDLKNINF

Signal peptide:

amino acids 1-19

Tyrosine kinase phosphorylation site:

amino acids 88-95

N-myristoylation sites:

amino acids 33-39, 35-41, 46-52

FIGURE 267

AGCGCCCGGCGTCGGGGCGGTAAAAGGCCGGCAGAAGGGAGGCACCTTGAGAAATGCTCTTTC
 CTCACAGGACCCAAGTTTCTTCACCATGGGGATGTGGTCCATTGGTGCAGGAGCCCTGGGGGGC
 TGTGCTTGGCATTGTCTGCTTGCCAAACACAGACGTGTTCTGTCCAAGCCCCAGAAAGCGG
 CCCTGGAGTACCTGGAGGATATAGACCTGAAAACACTGGAGAAGGAACCAAGGACTTTCAAA
 GCAAAGGAGCTATGGGAAAAAAATGGAGCTGTGATTATGGCCGTGCGGAGGCCAGGCTGTTT
 CCTCTGTGAGAGGAAGCTGCGGATCTGTCTCCTGAAAAGCATGTTGGACCAGCTGGGCG
 TCCCCCTCTATGCAGTGGTAAAGGAGCACATCAGGACTGAAGTGAAGGATTTCCAGCCTTAT
 TTCAAAGGAGAAATCTTCTGGATGAAAAGAAAAAGTTCTATGGTCCACAAAGGCGGAAGAT
 GATGTTTATGGGATTTATCCGTCTGGGAGTGTGGTACAACCTTCTCCGAGCCTGGAACGGAG
 GCTTCTCTGGAACCTGGAAGGAGAAGGCTTCATCCTTGGGGAGTTTTCGTGGTGGGATCA
 GGAAAGCAGGGCATTCTTCTTGAGCACCGAGAAAAAGATTTGGAGACAAAGTAAACCTACT
 TTCTGTTCTGGAAGCTGCTAAGATGATCAACCACAGACTTTGGCCTCAGAGAAAAATGAT
 TGTGTGAAACTGCCCAGCTCAGGGATAACCAGGGACATTACCTGTGTTTCATGGGATGTATT
 GTTTCACCTCGTGTCCCTAAGGAGTGAGAAACCCATTATATACTCTACTCTCAGTATGGATTA
 TTAATGTATTTAATATTCTGTTTAGGCCCACTAAGGCAAAATAGCCCCAAAAACAAGACTGA
 CAAAATCTGAAAACTAATGAGGATTATTAAGCTAAACCTGGGAAATAGGAGGCTTAAAA
 TTGACTGCCAGGCTGGGTGCAGTGGCTCACACCTGTAATCCAGCACTTTGGGAGGCCAAGG
 TGAGCAAGTCACTTGAGGTCGGGAGTTCGAGACCAGCCTGAGCAACATGGCGAAACCCCGTC
 TCTACTAAAAATACAAAAATCACCCGGGTGTGGTGGCAGGCACCTGTAGTCCCAGCTACCCG
 GGAGGCTGAGGCAGGAGAATCACTTGAACTGGGAGGTGGAGGTTGCGGTGAGCTGAGATCA
 CACCACTGTATTCCAGCCTGGGTGACTGAGACTCTAACTAA

FIGURE 268

MSFLQDPSFFTGMWWSIGAGALGAAALALLANTDVFLSKPQKALEYLEDIDLKTLEKEPR
TFKAKELWEKNGAVIMAVRRPGCFLCREEADLSSLKSMLDQLGVPLYAVVKEHIRTEVKDF
QPYFKGEIFLDEKKKFYGPQRRKMMFMGFIRLGWVYNFFRAWNGGFSGNLEGEFILGGVFV
VGSGKQGILLEHREKEFGDKVNLLSVLEAAKMIKPQTLASEKK

0991131 11601
10911 1211660

FIGURE 269

ACGGACCGAGGGTTCGAGGGAGGGACACGGACCAGGAACCTGAGCTAGGTCAAAGACGCCCC
GGCCAGGTGCCCCGTGCGAGGTGCCCTGGCCGAGATGCGGTAGGAGGGGCGAGCGCGAGA
AGCCCCCTTCCTCGGCGCTGCCAACCCGCCACCCAGCCCATGGCGAACCCGGGCTGGGGCTG
CTTCTGGCGCTGGGCCTGCCGTTCTCTGCTGGCCGCTGGGGCCGAGCCTGGGGGCAAATACA
GACCACTTCTGCAAAATGAGAATAGCACTGTTTTGCCCTTCATCCACCAGCTCCAGCTCCGATG
GCAACCTGCGTCCGGAAGCCATCACTGCTATCATCGTGGTCTTCTCCCTCTTGGCTGCCTTG
CTCCTGGCTGTGGGGCTGGCACTGTTGGTGCGGAAGCTTCGGGAGAAGCGGCAGACGGAGGG
CACCTACCGGCCAGTAGCGAGGAGCAGTTCTCCCATGCAGCCGAGGCCCGGGCCCCCTCAGG
ACTCCAAGGAGACGGTGCAGGGCTGCCTGCCCATCTAGGTCCCCCTCTCTGCATCTGTCTCC
CTTCATTGCTGTGTGACCTTGGGGAAGGCAGTGCCCTCTCTGGGCAGTCAGATCCACCCAG
TGCTTAATAGCAGGGAAGAAGGTACTTCAAAGACTCTGCCCTGAGGTCAAGAGAGGATGGG
GCTATTCACTTTTATATATTTATATAAAATTAGTAGTGAGATGTAAAAAAAAAAAAAAAAA

0901181 111501

270/330

FIGURE 270

MANPGLGLLLALGLPFLLARWGRAWGQIQTTSANENSTVLPSSSTSSSDGNLRPEAITAIIV
VFSLLAALLLAVGLALLVRKLREKRQTEGTYRPSSEEQFSHAAEARAPQDSKETVQGCLPI

099131.11601

FIGURE 271

AATATATCATCTATTTATCATTAAATCAATAATGTATTCTTTATTCCAATAACATTGGGTT
TTGGGATTTTAATTTTCAAACACAGCAGAAATGACATTTTCTGTCACTATTATTATGTG
GTATGTGAAGCTATTTGGAGATCCAATTCAGGAAGCAACACATTGGAGAATGGCTACTTTCT
ATCAAGAAATAAAGAGAACCACAGTCAACCCACACAATCATCTTTAGAAGACAGTGTGACTC
CTACCAAAGCTGTCAAACCACAGGCAAGGGCATAGTTAAAGGACGGAATCTTGACTCAAGA
GGGTAAATTCCTTGGTGCTGAAGCCTGGGGCAGGGGTGTAAAGAAAAACACTTAGATTCAATG
ATTGTAAATTTAAGGCAAATACACATATTAGTATTACCTTAGTGTAATGTATCCCTGTCATA
TATACAATAAGGTGAAATTATAAGTACCCTATGCAGTTGGCTGGACAGTTCTAAATTGGACT
TTATTAATTTTAAAAATCAGTAACTGATTTATCACTGGCTATGTGCTTAGATCTACAGGAGA
TCATATAATTTGATACAAATAAAAGAAAAGTGTCTCTCCCCTTACAGAATTGACATTTTAA
ATGCGATACAGTTAGAATAGGAAATATGACATTAGAAAGGAAGAATGACAGGGAGAAAGGAA
AGAAGGGAAAATGTTGCCAAGGAAAAAAAAA

FIGURE 272

MTFFLSLLLLLVCEAIWRSNSGSNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKTTGK
GIVKGRNLDSRGLILGAEAWGRGVKKNT

099181-11601

FIGURE 273

GCCAGGAATAACTAGAGAGGAACA**ATG**GGGTATTACTCAGAGGTTTTGTTTTCTCTTAGTTCT
 GTGCCCTGCTGCCACCACTCAAATACTTCTTCATTAAAGCTGAATAATAATGGCTTTGAAGATA
 TTGTCATTGTTATAGATCCTAGTGTGCCAGAAGTAAAAAATAATGAACAAATAGAGGAT
 ATGGTGACTACAGCTTCTACGTACCTGTTTGAAGCCACAGAAAAAGATTTTTTTCAAAAA
 TGTATCTATATTAAATCTTGAGAAATTTGGAAGGAAATTCCTCAGTACAAAAGGCCAAAACATG
 AAAACCATAAACATGCTGATGTTATAGTTGCACCACTACACTCCAGGTAGAGATGAACCA
 TACACCAAGCAGTTACAGAAATTTGGAGAGAAAGGCCGAATACATTCACTTCAACCCGTACCT
 TCTACTTTGGAAAAAAACAAATGAATATGGACCACCAAGGCAAACTGTTTGTCCATGAGTGGG
 CTCACCTCCGGTGGGGAGTGTGATGAGTACAATGAAGATCAGCCTTCTACCGTGCTAAG
 TCAAAAAAATCGAAGCAACAAGGTGTCCCGCAGGTATCTCTGGTAGAAAATAGAGTTTATAA
 GTGTCAAGGAGGCAGCTGTCTTAGTAGAGCATGCAGAATTGATTCTACAAACAAATCTGTATG
 GAAAAGATTGTCAATTCTTCCCTGATAAAGTACAAAACAGAAAAGCATCCATAATGTTTTATG
 CAAAGATTGTGATCTGTTGTTGTAATTTTGTAAACGAAAAAACCCATAATCAAGAAAGCTCCAG
 CCTACAAAACATAAAGTGCRAATTTAGAAAGTACATGGGAGGTGATTAGCAATCTCAGGATT
 TTA AAAACACCATTACCCATGGTGACACCACCTCTCCACCTGTCTTCTCATTCCTGAAAGTC
 AGTCGAAAGAAATGTGTGCTTAGTTCTTGATAAGTCTCGGAAGCATGGGGGGTGAAGACCCCT
 AAATCGAAATGATCAAGCAGCAAAACATTCCTGTCGAGACTGTTGAAGATGGATCCCTGGG
 TGGGATGGTTCACTTTGTATGATCTGCACATATTGTCTAAAGCTAATTCGAAATTA AAAAGC
 ACTGATGAAGAAGAACACACTCATGGCAGGATTACCTCATATCTCTGGGAGAACTTCAT
 CTGCTCTCGAATTAATATGCAATTTCAAGTGATTGGAGAGCTACATTCCEAACTCCAGTGGAT
 CCGAGTACTGCTGCTGACTGATGGGGAGGATAACACTCGAAGTTCTTGATTTGATGAAGTG
 AAACAAGTGGGGCCATTGTTCATTTTATTGCTTTGGGAAGAGCTGCTGATGAAGCAATAT
 ACAGATGAGCAAGATTAACAGGAGGAAGTCATTTTTATGTTTCAGATGAAGCTCAGAACATG
 GCCTCATTGATGCTTTTGGGGCTCTTACATCAGGAAATACCTGATCTCTCCAGAGTCCCTT
 CAGCTCGAAAGTAAAGGATTAACACTGAATAGTAATGCCTGGATGAACACACTGCTCATAT
 TGATAGTACAGTGGGAAGGACACGTTCTTCTCATACATGGAACAGCTGCTCCTCCAGTA
 TTTCTCTCTGGGATCCAGTGGAAACAATAATGGAAAAATTTACAGTGGATGCAACTTCAAA
 ATGGCCTATCTCAGTATTCCAGGAACATGCAAGGTGGGCACTTGGGCATACAAATCTTCAAGC
 CAAAGCGAACCAGAAACATTAACATTTACAGTAACCTCTCGAGCAGCAAAATCTTCTGTGTC
 CTCCAAATCAGAGTGAATGCTAAAATGAATAAGGACGTAAACAGTTTCCCAGGCCAATGATT
 GTTTACGCAAGAAATTTACAAGGATATGTACCTGTCTTGGAGCCAATGTGACTGCTTTTCAT
 TGAATCAGAGAATGGACATACAGAAGTTTGGAACTTTTGGATAATGGTGCAGGCGCTGATT
 CTTTCAAGAATGATGGAGTCTACTCCAGGTATTTTACAGCATATACAGAAAAATGGCAGATAT
 AGCTTAAAGTTTCGGGCTCATGGAGGAGCAAACTGCCAGGCTAAAATTACGGGCTCCACT
 GAATAGAGCCGCTACATACCAGGCTGGGTAGTGAACGGGGAAATTTGAAGCAAAACCCGCCAA
 GACCTGAAATTTGATGAGGATACCTCAGACCACCTTTGGAGGATTTCAGCCGAACAGCATCCGGA
 GGTGCATTTGTGGTATCACAAGTCCCAAGCCTTCCCTTGCTGACCAATACCCACCAAGTCA
 AATCACAGACCTTGATGCCACAGTTCACTGAGGATAAAGATTATTTCTTACATGGACAGCACCG
 GAGATAAATTTTGATGTTGGAAAAAGTTCAACGTTATATCATAGAATAAGTGCAAGTATTTCTT
 GATCTAAGAGACAGTTTGTATGATGCTCTTCAAGTAAATACTACTGATCTGTCAACCAAGGA
 GGCCAACTCCAAGGAAGCTTTGCATTTAAACAGAAAAATATCTCAGAGAAATAATGCAACCC
 ACATATTTTATGCCATTTAAAGATATAGATAAAAGCAATTTGACATCAAAAGTATCCAACTT
 GCACAAGTAACCTTTGTTTATCCCTCAAGCAAACTCTGATGACATTGATCTTACACTATCTC
 TACTCCTACTCCTACTCCTGATAAAAGTCATAATTTCTGGAGTTAATATTTCTACGCTGGTAT
 TGTCTGTGCTGGGCTGTTGTAATTTGTTAACTTTATTTTAAAGTACCACCTTT**TGA**ACCTTA
 ACGAAGAAAAAATCTTCAAGTAGACCTAGAAGAGAGTTTAAAAAAACAAAACATGTAAGT
 AAAGGATATTTCTGAATCTTAAATTCATCCCTATGCTGTGATCAAACTCATAAAAATAAT
 TTAAGATGTGCGAAAAGGATACTTTGATTAATAAAAAACACTCATGGATATGTAAAAAATCT
 CAAGATTAATAATTAATAGTTTTCATTTATTTGTTATTTTGTGAAGAAATAGTGAATGAAC
 AAAGATCCCTTTTTCTATACGTACCTGGTTGTATATTTTGTGTAACAGCTTTTCTGTAAT
 GATATTTCAAAATTTGCATCAAGAAATTAATAATCATCTATCTGAGTGTCAAAATCAAGTAAA
 GGAGAGCAAAATAAACAACTTTGGAAAAA AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

03091131.111601
 111601

MGLFRGFVFFLLVCLLHQNSTSFIKLNNGGFEDIVIVIDPSVPEDEKIEQIEDMVTTASTY
LFEATEKRFFFKNVSILIPENWKENPQYKRPHENHKKHADVIVAPPTLPGRDEPYTKQFTEC
GEKGEYIHFTPDLLLKKQNEYGPPGKLFVHEWAHLRWGVFDEYNEDQPFYRAKSKKIEATR
CSAGISGRNRVYKQGGSCLSRACRIDSTTKLYGKDCQFFPDVKVQTEKASIMFMQSIDSVVE
FCNEKTHNQEAPSLQNIKCNFRSTWEVISNSEDFKNTIPMVTPPPPVFSLLKISQRIVCLV
LDKSGSMGGKDRLNRMNQAAKHFLLLQTVENGSWFGMVHFDSTATIVNKLIQIKSSDERNTLM
AGLPTYPLGGTSCSGIKYAFQVIGELHSQLDGSEVLLLTGDGEDNTASSCIDEVKQSGAIVH
FIALGRAADEAVIEMSKITGGSHFYVSDEAQNNGLIDAFGALTSNGTDLSQLQLESKGLT
LNSNAWMNDTVIIDSTVGKDTFFLITWNLSLPPSISLWDPSTIMENFTVDATSKMAYLSIPG
TAKVGTWAYNLQAKANPETLTTITVSRAANSSVPPITVNAKMKNKDVNSFPSPMIVYAEILQG
YVPVLGANVTAFIESQNGHTEVLELLDNGAGADSFKNDGVYSRYFTAYTENGRYSLKVRHG
GANTARLKLRPPLNRAAYIPGWVNVGEIEANPPRPEIDEDTQTTLEDFSRTASGGAFVVSQV
PSLPLPDQYPPSQITDLBATVHGEKIIILTWTAPGDNFDVGKVQRYIRISASIDLDRDSFDD
ALQNPTNDTSLSPKANSKESFAKPENISEENATHIFIAIKSIDKSNLTSKVSNIAQVTLFIP
QANPDDIDTPTPTPTPTPKSHNSGVNISTLVLVSGVSVVIVNFIILSTTI

amino acids 1-21

amino acids 284-300, 617-633

amino acids 469-491, 476-498

amino acids 20-24, 75-79, 340-344, 504-508, 542-546, 588-592,
628-632, 811-815, 832-836, 837-841, 852-856, 896-900

FIGURE 275

CTCCTTAGGTGGAACCCCTGGGAGTAGAGTACTGACAGCAAAAGACCGGGAAGACCATACGTCCCCG
GGCAGGGGTGACAAACAGGTGTCATCTTTTGTATCTCGTGTGTGGCTGCCCTTCATTTTCAAGGAAGC
ACGCCAAGGTAATTTTGACCCAGAGGAGCAATGATGTAGCCACCTCTCAACCTTCCTTTGTAAAC
CCGAGTTATGCCAGGATTTTACTAGAGAGTGTCAACTCAACCAGCAAGCGGCTCCTTCGGCTTAACTT
TGTGTTGGAGGAGAACCTTTGTGGGGTGTGCTTCTTAGCAGTGTCTCAGAATGACTTGTCTGA
GGGTGGACCAAGAAGAAAGGAAAGGTCCTCTTGTCTGTGGCTGCACATCAGGAAGGCTGTGTATGGG
AATGAAGGTGAAACTTTTGAGATTTTCACTTCAGTCATTGCTTCTGCTCGAAGATCATCTTTTAAAAA
GTAGAGAAAGTGTCTGTGTGGTGGTAACTCCAAGAGGCAGAAGCTCGTTCTAGAAGGAATGGATG
CAAGCAGCTCCGGGGGCCCAACAGCATGCTTCTGTGTGCTAGCCAGGGAAGCCCTTCCTGTGGG
GCCCGCGCTTTGAGGATGCCACCGGTTCTGGACGATGGCTGATTCTCTGATGATGATGGTTTCGCC
GGGGGCTGCTTGGCTGGATTTCGCCGGGTGGTGGTTTGTGTGTGCTCCTCTGCTGTGCTATCTCTGT
CCTGTACATGTTGGCTGTCAACCCCAAGGTTGACGAGGAGCAGCTGGCAGCTGCCAGGGCCAAACAGC
CCACCGGGGAAGAGGGGTTCCRAGGCCCTCTTCAGGATGGGAGGAGCAGCCCAACTCAGCTGA
CGACGCTGAAGCGGAGATCGCACGCTCAAGGAGAGCTCAGGAGGAGATGAGCAGCTCAGGA
TGGCAGCTACCAACCGCAGCATGCTGCTGGCTGGCTGTGACAGGAGCCCGCAGAGAAACCCAG
GCCAGCTCTCTGGCTTCTGTCACTCGCAGTGGACAAGGACAGAGTGAATGCTGGCTCAAGCTGG
CCACAGAGTATGACAGCAGTGCCCTTTCGATAGCTTTACTCTACAGAAGGTGTACCAGCTGGAGACTGG
CCTTACCAGCCACCCCGAGGAGAAGCCTGTGAGGAAGGACAAGCGGGATGAGTTGGTGGAGCCATT
GAATCAGCCCTTGAGACCTGGAACATCTCGAGAGAACAGCCCCAATCACCCTCTTACAGCGCTCT
CTGATTTTCATAGAGGGATCTACCGAACAGAAAGGGACAAAGGGACATTTGATGAGCTACCTTTCAA
AGGGGACCAACAAACGAGATTCAAACGGCTCATCTTATTTTCGACCATTCAGCCCCATTCAGGAAGT
AAAAATGAAAGGCTCAACATGGCCACACGCTTATCAATGTTATCGTGCTCTAGACAAAAGGGTGG
ACAAGTTTCGGCGAGTTTCATGCGAATAATTCAGGGAGATGTGCATTCAGCAGAGTTGGGAGAGTCCATCT
CAGCTGTTGTTTACTTTTGGGAAGAAGAATAAATGAGCTCAAAGGAATATGAGAAAACATCTCCAA
GCTGCCAACTTCAGCAATTTTACTCTCAGTCGAGTGAAGAGATTTCTTCGGGAGAGGAGCTTG
ATGTTGAGAGCCGCTCTCGGAAGGGAAGCAAGCTCTTCTCTTTTCTGTGATGTGGACATCTACTTT
CACATCTGAATTCCTCAATACGTTGAGGCTGAATACACAGCCAGGGAAGAAGTTATTTATCGAGTT
CTTTTCAGTCAGTACAATCCTGGCATATAATACGGCCACCATGATGAGTCCCTCCTTGGAAACAGC
AGCTGGTCAATAAGAAGGAACCTGGATTTTGGAGAGACTTTGGATTTGGGATGACGTGTCAAGTATCG
GTCAGACTTCATCAATATAGTGGGTGTTGATCTGGACATCAAAGGCTGGGGCGGAGAGGATGTGCAC
CTTTATCGCAAGATATCTCCACAGCAACCTCATAGTGGTACGGAGCCCTGTGCGAGGACTCTCCACC
TCTGGCATGAGAAGGCTCGATGGACGAGCTGACCCCGCAGCAGTACAAGATGTGCATCGAGTCCAA
GGCCATGAACCGGCGATCCCGAGGCCAGCTGGGCATGCTGTGTTTACGAGCAGATAGAGGCTCAC
CTTCGCAAAACAGAAACAGAGACAAGTAGCAAAAAAACAAGCACTCCACAGAGAAGGATTTGGGGAGA
CACTTTTTCTTCTTCTTGTGCAATTAAGTGAAGTGGCTGCAACAGAGAAAAGACTTCATTAAGGAGCG
ACAAAAGAAATGTGACATGATGGTCAGAGATGAGAAAGCTCCGATTTCTCTCTTGGGCTTTTAC
ACAGAAATCAAAATCTCCGCTTTCGCTGCAAAAGTAAACCAAGTTGACCTGTGAGGCTCTGACAT
AAGGCAGAAATGCTTTGAGATATATAAGCCTAATGGTGTGGAGGTTTGTGAGTGGTTTACAATACAT
GAGACCTGTTGTTTGTGTGCTCATTTGAAATATTTCATGATTAAAGACAGTTTGTGAAAATTTTCAAT
TAGCATGAAAGGCAAGCATATTTCTCTCATATGAATGAGCCTATCAGCAGGGCTCTAGTTTCTAGG
AATGCTAAAATATCAGAAGGCAAGGAGAGGATAGGCTTATATGATACTAGTGAGTACATTAAGTA
AAAATAAATGGACAGAAAAGAAAAGAAACCATAAATCTGTGTCATATTTCCCAAGATTAACCA
AAAATAATCTGCTTATGTTTGTGTTGCTCTTTTAACTGTCTCCGTTTCTTTCTTTTATTTAAAAAT
GCATTTTTTCTCTTGTGAGTTATAGTCTGCTTATTTAATTAACCATTTTGAAGGCTTACAAGAGA
GCACAAGTTGGCTACATTTTATATTTTTTAAAGAAGATACTTTGAGATGCATTAAGGAACCTTCA
GTTCAAAGCATCAATTTGATGCCATATCCAAGGACCAATGCTCATTTCTGTCAGGCAGTGAAT
CTCGAGCATTCAGCATAGGAGGATGCTTTGATACATACAGATACAGATATCTTCTGAA
GAGTATTTCCAAGAGGAGCACTGAACACTGGAGCAAAAGAAATGACATCTTCTGCTTTACAGAA
AAGGAACACTCACTGAGTGGTGATATCGTGATGTACCTAAAAGTCAGAAACCACTTTTCTCTCA
GAAGTAGGGACGGCTTTCTTACTGTTTAAATAAACCAAGTATACCGTGTGACCAACCAATCTCT
TTTCAAAACAGGCTGCTCCTTGGCTTCTGGCTTCCATAGAAGAAATGGAGAAAATATATATAT
ATATATATATATGTGGAAGATCAATCCATCTGCCAGAACTAGTGGGATGGAGTTTGTGTCTACAT
GTTATCCACCCAGGAGCTGGAAGTAACCTGAATTTATTTTAAATTAAGCAGTCTACTCAATCA
CCAAGATGCTTTGAAAAATGCAATTTTATTAACATTTCAAACATTTTTTAAAAATTAATACAGTTA
ACATAGAGTGGTTTCTTCATCTCATGTGAAATTTATAGCCAGCAGGATGCATGAGCTAATTTATCT
CTTTGAGTCTTGTCTGTGTTGCTCAAGTAAACTCATGTTTAAAAAGGCTTCAAGAACATCTCAAGC
TGTTGGTGTGTTAAAAATGCATTTGATTTGTTTGTACTGGTGTGTTTATGAATTTTAAATAAACAG
AGGCCATGAATGGAAGGTGGTATGTCACAGCTAATAAAATATGATTTGTGGATATGAA

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FIGURE 276

MMVRRGLLAWISRVVLLVLLCCAISVLYMLACTPKGDEEQIALPRANSPTGKEGYQAVLQ
EWEEQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGDRSPPEKTQADLLAFL
HSQVDKAEVNAGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPPEKPVRKDKRDELVEAIES
ALETLNNPAENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLILFRPFSP
MKVKNEKLNMANLINVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFGKEEINEVK
GILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNCR
LNTQPGKKVFYPVLFSEQYNPGIYGHHDVPPLEQQLVIKKETGFWRDFGFGMTCQYRSDFI
NIGGFDDIKGWGGEDVHLYRKYLHSNLIVVRTPVGRGLFHLWHEKRCMDELTPEQYKMCMQS
KAMNEASHGQLGMLVFRHEIEAHLRKQKQKTSSKKT

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FIGURE 277

GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTTCATGCTGAACTCTGTCAACC
 AGGTGCAGAAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCAT
 ATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA
 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGGGT
 ATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCTGCTGTTGAGGTGC
 AATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGACCAAACT
 CTGGAATTTTTAAAAATCCCTTCCACACTTGCAACCACCATGGACCCATCTGTGCCCATCTG
 GATTATTATATTTGGTGTGATATTTGCATCATCATAGTTGCAATTGCACTACTGATTTTAT
 CAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGATGACGCTGAAGAT
 AAGTGTGAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCCCTGGACATGAAGGG
 GGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGGCTCACCCCTCTCTGAAGGGCTGT
 GTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTGTGTGACTGCTGAGCATCCTGAAATA
 CCAAGAGCAGATCATATATTTTGTTCACCATTCTTCTTTGTAATAAATTTTGAATGTGCT
 TGAAAGTGAAAAGCAATCAATTATACCCACCAACACCACTGAAATCATAAGCTATTACAGAC
 TCAAAATATTTCAAAATATTTTCTGACAGTATAGTGATAAATGTGGTCATGTGGTATTTG
 TAGTTATTGATTTAAGCATTTTTAGAAATAAGATCAGGCATATGTATATATTTTACACTTC
 AAAGACCTAAGGAAAAATAAATTTCCAGTGGAGAATACATATAATATGGTGTAGAAATCAT
 TGAAAATGGATCCTTTTTGACGATCACTTATATCACTCTGTATATGACTAAGTAACAAAAG
 TGAGAAGTAATTATTGTAATGGATGGATAAAAATGGAATTACTCATATACAGGGTGGAATT
 TTATCTGTTATCACACCAACAGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGAC
 AATTCTATTGTGACCATTCTACAATTGTAAAGTCCAATCTGTGCCTAACTTAATAAAG
 TAATAATCATCTCTTTTTAAAAA

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FIGURE 278

MLWLFLFLVTAIHAELCQPGAENAFKVRLSIRTALGDKAYAWDTNEEYLFKAMVAFSMRKVP
NREATESHVLLCNVTQRVSFVVTDPKSNHTLPAVEVQSAIRMKNKRINNAFFLNDQTL
FLKIPSTLAPPMDSVPWIIIFGVIFCIIIVAIALLLSGIWQRRRNKEPSEVDDAEDKC
ENMITIENGIPSDPLDMKGGILMMP

DECEMBER

FIGURE 279

AACTCAAACCTCTCTCTCTGGGAAAACGCGGTGCTTGCTCCTCCCGAGTGCCCTTGGCAGG
 GTGTTGGAGCCCTCGGTCTGCCCCGTCCGGTCTCTGGGGCCAAGGCTGGGTTTCCCTC**ATGT**
 ATGGCAAGAGCTCTACTCGTGCGGTGCTTCTTCTCCTTGGCATACAGCTCACAGCTCTTTGG
 CCTATAGCAGCTGTGGAAATTTATACCTCCCGGTGCTGGAGGCTGTTAATGGACAGATGC
 TCGGTTAAATGCACTTTCTCCAGCTTTGCCCTGTGGGTGATGCTCTAACAGTGACCTGGA
 ATTTTCGTCCCTAGACGGGGGACCTGAGCAGTTTGTATTCTACTACCACATAGATCCCTTC
 CAACCCATGAGTGGGCGGTTTAAAGACCGGGTGCTTTGGGATGGGAATCCTGAGCGGTACGA
 TGCCTCCATCCTTCTCTGGAACTGCAGTTCGACGACAATGGGACATACACCTGCCAGGTGA
 AGAACCACCTGATGTTGATGGGGTGATAGGGGAGATCCGGCTCAGCGTCGTGCACACTGTA
 CGCTTCTCTGAGATCCACTTCTGGCTCTGGCCATTGGCTCTGCCTGTGCACTGATGATCAT
 AATAGTAATTGTAGTGGTCTCTTCCAGCATTACCGGAAAAAGCGATGGGCCGAAAGAGCTC
 ATAAAGTGGTGGAGATAAAATCAAAAGAAGAGGAAAGGCTCAACCAAGAGAAAAAGGTCTCT
 GTTTATTTAGAAGACACAGAC**TAA**CAATTTTAGATGGAAGCTGAGATGATTTCCAAGAACA
 GAACCTAGTATTTCTTGAAGTTAATGGAACTTTTCTTTGGCTTTTCCAGTTGTGACCCGT
 TTTCCAACCACTTCTGCAGCATATTAGATTCTAGACAAGCAACACCCCTCTGGAGCCAGCAC
 AGTGCTCCTCCATATACCAGTCATACACAGCCTCATTATTAAGGTCTTATTTAATTTCAGA
 GTGTAAATTTTTCAAGTGCTCATTAGGTTTTATAAACAAGAAGCTACATTTTGGCCCTTAA
 GACACTACTTACAGTGTTATGACTTGTATACACATATATTGGTATCAAAGGGGATAAAAGCC
 AATTTGCTCTGTACATTTCCTTTACGTATTTCTTTAGCAGCACTTCTGTACTAAAGTTA
 ATGTGTTACTCTCTTCCCTCCACATTTCTCAATTAAAGGTGAGCTAAGCCTCCTCGGTG
 TTCTTGATTAAACAGTAAATCCTAAATTCAAAGTGTAAATGACATTTTTATTTTTATGTCTC
 TCCTTAACTATGAGACACATCTTGTTTTACTGAATTTCTTTCAATATTCAGGTGATAGATT
 TTTGTGC

FIGURE 280

MYGKSSTRAVLLLLLGIQLTALWPAAVEIYTSRVLEAVNGTDARLKCTFSSFAPVGDALTVT
WNFRPLDGGFEQFVFYYHIDFFQPMSGRFKDRVSWDGNPERYDASILLWKLQFDDNGTYTCQ
VKNPPDVGVGIEIRLSVVHTVRFSEIHFLALAGSACALMIIIVIVVVLQHYRKKRWAER
AHKVVEIKSKEERLNQEKKVSVYLEDTD

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FIGURE 281

GCATTTTGTCTGTGCTCCCTGATCTTCAGGTCACCACCAATGAAGTTCTTAGCAGTCCTGGT
ACTCTTGGGAGTTTCCATCTTTCTGGTCTCTGCCCAGAATCCGACAACAGCTGCTCCAGCTG
ACACGTATCCAGCTACTGGTCCTGCTGATGATGAAGCCCCTGATGCTGAAACCACTGCTGCT
GCAACCACTGCGACCACTGCTGCTCCTACCACTGCAACCACCGCTGCTTCTACCACTGCTCG
TAAAGACATTCCAGTTTTACCCAAATGGGTGGGGATCTCCCGAATGGTAGAGTGTGTCCCT
GAGATGGAATCAGCTTGAGTCTTCTGCAATTGGTCACAACATTCATGCTTCCTGTGATTTT
ATCCAACACTACTTACCTTGCTACGATATCCCCCTTATCTCTAATCAGTTTATTTTCTTTCAA
ATAAAAAATAACTATGAGCAACATAAAAAAAAAAAAAA

FIGURE 282

MKFLAVLVLLGVSI FLVSAQNPTTAAPADTYPATGPADDEAPDAETTAAATTATTAAPTAT
TAASTTARKDIPVLPKWVGDL PNGRVCP

FIGURE 283

GGACTCTGAAGGTCCCAAGCAGCTGCTGAGGCCCCAAGGAAGTGGTTCCAACCTTGGACCC
 CTAGGGGTCTGGATTTGCTGGTTAACAAGATAACCTGAGGGCAGGACCCCATAGGGGA**ATGC**
 TACCTCCTGCCCTTCCACCTGCCCTGGTGTTCACGGTGGCCTGGTCCCTCCTTGCCGAGAGA
 GTGTCTGGGTGAGGACGCAGAGGACGCTCACAGACTCCAGCCCTTTGTTACCGAGAGGAC
 ACTTGGCAAGGTCCAGCGATGGTCCGGAGTCCACACACAGACTGGCGGCAGGGCAGGAGGGG
 GACAGTTCTGTTGTGCTTGGTTGGACAGTAAGAGGGTCTTGCCAGTCCAGGGTGGGGGGCG
 GCAAACCTCCATAAAGAACCAGAGGGTCTGGGCCCCGGCCACAGAGTCATCTGCCAGCTCCT
 CTGCTGCTGGCCAGTGGGAGTGGCACGAGGTGGGGCTTTGTGCCAGT**TAA**AACCACAGGCTGG
 ATTTGCCTGCGGGCCATGGTCCCTGTCTAGGGCAGCAATTCTCAACCTTCTTGCTCTCAGGA
 CCCCAAAGAGCTTTCATTGTATCTATTGATTTTTACCACATTAGCAATTTAAACTGAGAAAT
 GGGCCGGGCACGGTGGCTCACGCCGTGTAATCCAGCACTTTGGGAGGCCGAGGCGGGTGGAT
 CACCTGAGATCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACCTTGTCTACTAAAAA
 TACAAAAAATTAGCCAGGCACAGTGGTGTGCACTGGTAGTCCAGTTACTCGGGAGGCTGAG
 GCAGAAAAATCGCTTGAACCCAGGAGCGGACGTTGCGGTGAGCCGAGATCGCGCCGCTGAT
 TCCAGCCTGGGCACAAAGAGTGAGACTCCATCTCACACA

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FIGURE 284

MLPPALPPALVFTVAWSLLAERVSWVRDAEDAHRLQPFVTERTLGKVQRWSGVHTQTGGRAG
GGQFCCAWLDSKRVLASPGWGAANSIKNQRVWAPATESSAQLCCWFPVGVARGGALCQ

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FIGURE 285

GTCATGCCAGTGCCTGCTCTGTGCCTGCTCTGGGCCCTGGCAATGGTGACCCGGCCTGCCTCA
 GCGGCCCCCATGGGCGGCCAGAACTGGCACAGCATGAGGAGCTGACCCTGCTCTTCCATGG
 GACCCTGCAGCTGGGCCAGGCCCTCAACGGTGTGTACAGGACCACGGAGGGACGGCTGACAA
 AGGCCAGGAACAGCCTGGGTCTCTATGGCCGCACAATAGAACTCCTGGGGCAGGAGGTGAGC
 CGGGGCCGGGATGCAGCCAGGAACTTCGGGCAAGCCTGTTGGAGACTCAGATGGAGGAGGA
 TATTCTGCAGCTGCAGGCAGAGGCCACAGCTGAGGTGCTGGGGGAGGTGGCCAGGCACAGA
 AGGTGCTACGGGACAGCGTGCAGCGGCTAGAAGTCCAGCTGAGGAGCGCCTGGCTGGGCCCT
 GCCTACCGAGAATTTGAGGTCTTAAAGGCTCACGCTGACAAGCAGAGCCACATCCTATGGGC
 CCTCACAGGCCACGTGCAGCGGCAGAGGCGGGAGATGGTGGCACAGCAGCATCGGCTGCGAC
 AGATCCAGGAGAGACTCCACACAGCGGCGCTCCAGCCTTGAATCTGCCTGGATGGAAGTGA
 GACCAATCATGCTGCAAGGAACACTTCCACGCCCCGTGAGGCCCTGTGCAGGGAGGAGCTG
 CCTGTTCACTGGGATCAGCCAGGGCGCCGGGCCCACTTCTGAGCACAGAGCAGAGACAGAC
 GCAGCGGGGACAAAGGCAGAGGATGTAGCCCCATTGGGGAGGGGTGGAGGAAGGACATGTA
 CCCTTTTCATGCCTACACACCCCTCATTAAGCAGAGTCGTGGCATTTCAAAAAAAAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAA

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 1091181-111601

286/330

FIGURE 286

MPVPALCLLWALAMVTRPASAAPMGGPELAQHEELTLLFHGTLQLGQALNGVYRTTEGRLTK
ARNSLGLYGRTIELLGQEVSRGRDAAQELRASLLETQMEEDILQLQAEATAEVLGEVAQAQK
VLRDSVQRLEVQLRSAWLGPAYREFEVLKAHADKQSHILWALTGHVQRQRREMVAQQHRLRQ
IQERLHTAALPA

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FIGURE 288

MAQQACPRAMAKNGLVICILVITLLLDQTTSHTSRLKARKHSKRRVRDKDGLKTQIEKLWT
EVNALKEIQALQTVCLRGTKVHKKCYLASEGLKHFHEANEDCISKGGILVIPRNSDEINALQ
DYGKRSLPGVNDFWLGINDMVTEGKFVDVNGIAISFLNWDRAQPNGGKRENCVLFSQSAQ GK
WSDEACRSSKRYICEFTIPK

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FIGURE 289

GCGAGGACCGGGTATAAGAAGCCTCGTGGCCTTGCCCGGGCAGCCGCAGGTTCCCCGCGCGC
 CCCGAGCCCCGCGCC**ATG**AAGCTCGCCGCCCTCCTGGGGCTCTGCGTGGCCCTGTCCTGCA
 GCTCCGCTGCTGCTTTCTTAGTGGGCTCGGCCAAGCCTGTGGCCAGCCTGTCGCTGCGCTG
 GAGTCGGCGGCGAGGCCGGGCGGGACCC**TG**GCCAACCCCTCGGCACCC**TCA**ACCCGCT
 GAAGCTCCTGCTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCAGAA**GT**
 GTGTGGCTGAGCTGGGTCCCCAGGCCGTGGGGGCCGTGAAGGCCCTGAAGGCCCTGCTGGGG
 GCCCTGACAGTGTTTGGCT**TGA**GCCGAGACTGGAGCATCTACACCTGAGGACAAGACGCTGCC
 CACCCGCGAGGGCTGAAAACCCCGCCGCGGGGAGGACCGTCCATCCCCTTCCCCGGCCCC**T**
 CTCATAAACGTGGTTAAGAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
 AAAAAAAAAA

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290/330

FIGURE 290

MKLAALLGLCVALSCSSAAAFVGSAPVAPVAALESAAEAGAGTLANPLGTNLNPLKLLLS
SLGIPVNHIEGSQKCVaelGPQAVGAVKALKALLGALTVFG

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FIGURE 291

TGAAGGACTTTTCCAGGACCCAAGGCCACACACTGGAAGTCTTGCAGCTGAAGGGAGGCAC
 CCTTGGCCTCCGCGAGCCGATC**CATGA**AGGTGGTGCCAAAGTCTCCTGCTCTCCGTCTCCTG
 GCACAGGTGTGGCTGGTACCCGGCTTGGCCCCAGTCTCAGTCGCCAGAGACCCAGGCCCC
 TCAGAACCCAGCAGCAGGGTAGTGCAGGCTCCAGGGAGGAAGAGGAAGATGAGCAGGAGG
 CCAGCGAGGAGAAGGCCGGTGAGGAAGAGAAGCCTGGCTGATGGCCAGCAGGCAGCAGCTT
 GCCAAGGAGACTTCAAACCTTCGGATTAGCCTGCTGCGAAAGATCTCCATGAGGCACGATGG
 CAACATGGTCTTCTCTCCATTTGGCATGTCTTGGCCATGACAGGCTTGATGCTGGGGGCCA
 CAGGGCCGACTGAAACCCAGATCAAGAGAGGGCTCCACTTGAGGCCCTGAAGCCACCAAG
 CCGGGGCTCCTGCCTTCCCTCTTTAAGGGACTCAGAGAGACCTCTCCCGCAACCTGGAAT
 GGGCCTCTCACAGGGGAGTTTGGCCTTCATCCACAAGGATTTTGATGTCAAAAGAGACTTTCT
 TCAATTTATCCAAGAGGTATTTTGATTACAGAGTGCCTGCTATGAATTTTCGCAATGCCTCA
 CAGGCCAAAAGGCTCATGAATCATTACATTAACAAAGAGACTCGGGGGAAAATCCCAAACCT
 GTTGTATGAGATTAATCCTGAAACCAAATTAATTTCTGTGGATTACATCTTGTCAAAGGGA
 AATGGTTGACCCCATTTGACCCTGTCTTCACCGAAGTCGACACTTTCACCTGGACAAGTAC
 AAGACCATTAAAGTGCCCATGATGTACGGTGCAGGCAAGTTTGCCTCCACCTTTGACAAGAA
 TTTTCGTTGTCTATGTCTCAAACCTGCCCTACCAAGGAAATGCCACCATGCTGGTGGTCTCA
 TGGAGAAAATGGGTGACCACCTCGCCCTTGAAGACTACCTGACCACAGCTTGGTGGAGACA
 TGGCTCAGAAACATGAAAACCCAGAAACATGGAAGTTTCTTCCGAAGTTCAAGCTAGATCA
 GAAGTATGAGATGCATGAGCTGCTTAGGCAGATGGGAATCAGAAGAATCTTCTACCCCTTTG
 CTGACCTTAGTGAACTCTCAGCTACTGGAAGAAATCTCCAAGTATCCAGGGTTTTACGAAGA
 ACAGTGATTGAAGTTGATGAAAGGGGCACTGAGGCAGTGGCAGGAATCTTGTGAGAAATTAC
 TGCTTATTCCATGCCTCCTGTCTCAAAAGTGAGACCGGCATTTCAATTCATGATCTATGAAG
 AAACCTCTGGAATGCTTCTGTTTCTGGGCAGGGTGGTGAATCCGACTCTCCTAT**TA**ATTGAGG
 ACATGCATAAGCACTTCGTGCTGTAGTAGATGCTGAATCTGAGGTATCAAACACACACAGGA
 TACCAGCAATGGATGGCAGGGGAGAGTGTCTCTTTGTTCTTAACCTAGTTTAGGGTGTCTC
 AAATAAATACAGTAGTCCCCACTTATCTGAGGGGGATACATTCAAAGACCCCCAGCAGATGC
 CTGAAACGGTGGACAGTGCTGAACCTTATATATATTTTTTCTACACATACATACCTATGAT
 AAAGTTAATTTATAAATTAGGCACAGTAAGAGATTAACAATAATAACAACATTAAGTAAAA
 TGAGTTACTTGAACGCAAGCACTGCAATACCATAACAGTCAAACCTGATTATAGAGAAGGCTA
 CTAAGTACTCATGGCGAGGAGCATAGACAGTGTGGAGACATTGGGCAAGGGGAGAATTCA
 CATCCTGGGTGGGACAGGACGGAGCATGCAAGATTCCATCCCACTACTCAGAATGGCATGC
 TGCTTAAGACTTTTAGATTGTTTATTCTGGAATTTTCATTAAATGTTTGGACCATGTT
 TGACCATGGTTAACTGAGCTGCAGAAAGCAAAACCATGGATGAAGGGAGGACTACTACAAAA
 GCATTAAATTGATACATATTTTTTAAAAAAAAAAAAAAAAAAAA

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FIGURE 292

MKVVP S L L L S V L L A Q V W L V P G L A P S P Q S P E T P A P Q N Q T S R V V Q A P R E E E E D E Q E A S E E K A G E
E E K A W L M A S R Q Q L A K E T S N F G F S L L R K I S M R H D G N M V F S P F G M S L A M T G L M L G A T G P T E T Q I
K R G L H L Q A L K P T K P G L L P S L F K G L R E T L S R N L E L G L S Q G S F A F I H K D F D V K E T F F N L S K R Y F
D T E C V P M N F R N A S Q A K R L M N H Y I N K E T R G K I P K L F D E I N P E T K L I L V D Y I L F K G K W L T P F D P
V F T E V D T F H L D K Y K T I K V P M M Y G A G K F A S T F D K N F R C H V L K L P Y Q G N A T M L V V L M E K M G D H L
A L E D Y L T T D L V E T W L R N M K T R N M E V F F P K F K L D Q K Y E M H E L L R Q M G I R R I F S P F A D L S E L S A
T G R N L Q V S R V L R R T V I E V D E R G T E A V A G I L S E I T A Y S M P P V I K V D R P F H F M I Y E E T S G M L L F
L G R V V N P T L L

FIGURE 293

CTGGGATCAGCCACTGCAGCTCCCTGAGCACTCTCTACAGAGACGCGGACCCAGACATGAG
GAGGCTCCTCCTGGTCACCAGCCTGGTGGTTGTGCTGCTGTGGGAGGCAGGTGCAGTCCCAG
CACCCAAGGTCCCTATCAAGATGCAAGTCAAACACTGGCCCTCAGAGCAGGACCCAGAGAAG
GCCTGGGGCGCCCGTGTGGTGGAGCCTCCGGAGAAGGACGACCAGCTGGTGGTGTGTTCCC
TGTCCAGAAGCCGAAACTCTTGACCACCGAGGAGAAGCCACGAGGTGAGGGCAGGGGCCCA
TCCTTCCAGGCACCAAGGCCTGGATGGAGACCGAGGACACCCTGGGCCGTGTCCTGAGTCCC
GAGCCCGACCATGACAGCCTGTACCACCCTCCGCCTGAGGAGGACCAGGGCGAGGAGAGGCC
CCGGTTGTGGGTGATGCCAATCACCAGGTGCTCCTGGGACCGGAGGAAGACCAAGACCACA
TCTACCACCCCAGTAGGGCTCCAGGGGCCATCACTGCCCCGCCCTGTCCAAGGCCAGG
CTGTTGGGACTGGGACCCTCCCTACCCTGCCCAGCTAGACAAATAAACCCAGCAGGCAAA
AAAAAAAAAAAAAA

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AGAAAGCTGCACTCTGTTGAGCTCCAGGGCGCAGTGGAGGGAGGGAGTGAAGGAGCTCTCTG
TACCCAAGGAAAGTGCAGCTGAGACTCAGACAAGATTACAATGAACCAACTCAGCTTCCTG
TGTTTCTCATAGCGACCACCAGAGGATGGAGTACAGATGAGGCTAATACTTACTTCAAGGAA
TGGACCTGTTCTTCGTCTCCATCTCTGCCAGAAGCTGCAAGGAAATCAAGACGAATGTCC
TAGTGCAATTGTATGGCCTGTATTTTCTCGCACTGAGAATGGTGTTATCTACCAGACCTTCT
GTGACATGACCTCTGGGGGTGGCGGTGGACCTGGTGCCAGCGTGCATGAGAATGACATG
CGTGGGAAGTGCACGGTGGCGGATCGCTGGTCCAGTCAGCAGGGCAGCAAAGCAGACTACCC
AGAGGGGGACGGCAACTGGGCCAACTACAACACCTTTGGATCTGCAGAGCGGGCCACGAGCG
ATGACTACAAGAACCTGGCTACTACGACATCCAGGCCAAGGACCTGGGCATCTGGCACGTG
CCCAATAAGTCCCCATGCAGCACTGGAGAAACAGCTCCCTGCTGAGGTACCGCACGGACAC
TGGCTTCCTCCAGACACTGGGACATAATCTGTTTGGCATCTACCAGAAATATCCAGTGAAT
ATGGAGAAGGAAAGTGTTGGACTGACAACGGCCCCGTGATCCCTGTGGTCTATGATTTTGGC
GACGCCCAGAAAAACAGCATCTTATTACTCACCTATGGCCAGCGGGAATTCACGCGGGATT
TGTTCAGTTTCAGGGTATTTAATAACGAGAGAGAGGCCAACGCCTTGTTGTCTGGAATGAGG
TCACCGGATGTAACACTGAGCATCACTGCATTGGTGGAGGAGGATACTTCCAGAGGCCAGT
CCCCAGCAGTGTGGAGATTTTCTGGTTTTGTATGGAGTGGATATGGAATCATGTTGGTTA
CAGCAGACGCCGTGAGATAACTGAGGCAGCTGTGCTCTTATCTATCGTTGAAGTTTGTG
GGAGGGAACCCAGACCTCTCTCCCAACCATGAGATCCCAAGATGGAGACAACATATCCCA
GTAGCTAGAATGTTAATGGCAGAAGAGAAAAACATAAATCATATTGACTCAAGAAAAAAA

FIGURE 296

MNQLSFLLFLIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRTEN
GVIYQTFCDMTSGGGWTLVASVHENDMRGKCTVGDRWSSQQGSKADYPEGDGNWANYNTFG
SAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLLRYRTDTGFLQTLGHNLFGI
YQKYPVKYGEKGCWTDNGPVI PVVYDFGDAQKTASYSPYQGQREFTAGFVQFRVFNNERAAN
ALCAGMRVTGCNTEHHCIGGGGYFPEASPQQCGDFSGFDWSGYGTHVGYSRSSREITEAAVLL
FYR

FIGURE 297

GCGGAGCCGGCGCCGGCTGCGCAGAGGAGCGCTCTCGCCGCCGCCACCTCGGCTGGGAGCC
CACGAGGCTGCCGCATCTGCCCTCGGAACA**ATG**GGACTCGGCGCGGAGGTGCTTGGGCCG
CGTGCTCTCTGGGACGCTGCAGTGCTAGCGTGCTGGGGCCGCCCATGAAAGCGCAGCC
ATGGCGGCATCTGCAAAATAGAGAATTCTGGGCTTCACACAACCTCCAGTGCTAACTCAAC
AGAGACTCTCAACATGTGCCTTCTGACCATACAAAATGAAACTTCCAACAGTACTGTGAAAC
CACCAACTTCAGTTGCCTCAGACTCCAGTAATACAACGGTCACCACCATGAAACCTACAGCG
GCATCTAATAACAACAACACAGGGATGGTCTCAACAATATGACTTCTACCACCTTAAAGTC
TACACCCAAAACAACAGTGTTTACAGAACACATCTCAGATATCAACATCCACATGACCG
TAACCCACAATAGTTCAGTGACATCTGCTGCTTACAGTAAACATCAACAACATATGCAT
TCTGAAGCAAGAAGAGATCAAAATTGTACTGGGAGCTTTGTGTGGTATTGTATTAAAC
GCTGGGAGTTTTATCTATTCTTTACATTGGATGCAAAATGTATTACTCAAGAAGAGGCATTTC
GGTATCGAACCATAGATGAACATGATGCCATCATT**TAA**GGAATCCATGGACCAAGGATGGA
ATACAGATTGATGCTGCCCTATCAATTAATTTTGGTTTATTAATAGTTTAAACAATATTTCT
CTTTTGA AAATAGTATAAACAGGCCATGCATATAATGTACAGTGTATTACGTAAATATGTA
AAGATTCTTCAAGGTAACAAGGGTTTGGTTTGAATAAACATCTGGATCTTATAGACCGT
TCATACAAATGGTTTTAGCAAGTTCATAGTAAGACAAACAAGTCCATCTTTTTTTTTTGCGT
GGGGTGGGGGCATTGGTCACATATGACCAGTAATTGAAAGACGTCATCACTGAAAGACAGAA
TGCCATCTGGGCATACAAATAAGAAGTTTGTACAGCACTCAGGATTTTGGGTATCTTTTGT
AGCTCACATAAAGAACTTCAGTGTCTTTTCAGAGCTGGATATATCTTAATTACTAATGCCACA
CAGAAATTATACATCAAACTAGACTGTAGAGCTAAGATTAATGAAGAAAACATCAACATTTTTG
TGCTTTAAACTGTAGTAGTTGGTCTAGAAAACAAATACTCC

FIGURE 298

MGLGARGAWAALLLGTQLQVLALLGAAHESAAMAASANIENSGLPNSSANSTETLQHVPSDH
TNETSNSTVKPPTSVDSSNTTVTTMKPTAASNTTTPGMVSTNMTSTTLKSTPKTTSVSQN
TSQISTSTMTVTHNSSVTSAASSVTITTTMHSEAKKGSKFDTGSFVGGIVLTLGVLSILYIG
CKMYYSRRGIRYRTIDEHDAII

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FIGURE 299

CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCCGG
 TCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCAGCG**ATG**CGCACCCTGTGGGGAGGC
 CTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCTGCTGGCGCTTCCGTGCTGCTGCTGGC
 GCAGCTGTGAGACGCCGCCAAGAATTTTCGAGGATGTGAGATGTAAATGTATCTGCCCTCCCT
 ATAAAGAAAATTTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTGTGATTGCCTT
 CATGTTGTGGAGCCCATGCCTGTGCGGGGCTGATGTAGAAGCATACTGTCTACGCTGTGA
 ATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTATAATTTATCTCTCCA
 TTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGAGCCCATACTGAAGAGG
 CGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATATTGGGGATCACCAGCCTTT
 TGCAATGCACAGCATGTGCTAGCCCGCTCCCGCAGTCGAGCCAAAGTGTGTAACAAGGTAG
 AATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCAGCGAAAGTCTGTCTTTGACCGG
 CATGTTGTCTCTCAGC**TAA**TTGGGAATTGAATTCAGGTGACTAGAAAGAAACAGGCAGACAA
 CTGGAAGAAGTACTGCTGGTTTTGCTGGGTTTCAATTTAATACCTTGTTGATTTTCAACACT
 GTTGCTGGAAGATTCAAACTGGAAGCAAAACTTGCTTGATTTTTTTTCTTGTTTAAACGTA
 ATAATAGAGACATTTTTAAAAGCACACAGCTCAAAGTCAGCCAATAAGTCTTTTCCTATTG
 TGACTTTTACTAATAAAAAATAAATCTGCCTGTAAATTATCTTGAAGTCTTTTACCTGGAACA
 AGCACTCTCTTTTACCACATAGTTTTAACTTGACTTTCAAGATAATTTTCAAGGTTTTTG
 TTGTTGTTGTTTTTGTGTTGTTTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGGTT
 AACAACTTTTTCAAGTCACTTTACTAAACAACTTTTGTAATAGACCTTACCTTCTATTT
 TCGAGTTTCATTTATATTTTGCAGTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTTG
 ACTTTTGCACGTGACTGTATTTATCTGGGTATCTGCTGTGTCTGCACCTCATGGTAAACGGGAT
 CTAAATGCCTGGTGGCTTTTACAAAAAGCAGATTTTCTTCATGTACTGTGATGTCTGATG
 CAATGCATCCTAGAACAAGTGGCCATTTGCTAGTTTACTCTAAAGACTAAACATAGTCTTG
 GTGTGTGTTGCTTACTCATCTTCTAGTACCTTTAAGGACAAATCCTAAGGACTTGGACACT
 TGCAATAAAGAAATTTTATTTTAAACCAAGCCTCCCTGGATTGATAATATATACACATTTG
 TCAGCATTTCCGGTCGTGGTGAGAGGCAGCTGTTTGAGCTCCAATATGTGCAGCTTTGAAC
 AGGGCTGGGGTTGTGGGTGCCTCTTCTGAAAGGTCTAACCATTATTGGATAACTGGGCTTTT
 TCTTCCATATGCCTCTTTGGAATGTAACAATAAAAAATAATTTTGAACATCA

FIGURE 300

MATLWGGLRLGSLLSLCLALSVLLLAQLSDAAKNFEDVRCKCICPPYKENSNGHIYNKNIS
QKDCDCLHVVEPMPVRGPDVEAYCLRCECKYEERSSVTIKVTIIIIYLSILGLLLLYMYLTL
VEPILKRRLFGHAQLIQSDDDIGDHQPFANAHDLARSRSRANVLNKVEYAQQRWKLQVQEQ
RKSVFDRHVVLS

FIGURE 301

GCACCTGCGACCACCGTGAGCAGTCAATGGCGTACTCCACAGTGCAGAGAGTCGCTCTGGCTT
CTGGGCTTGTCCTGGCTCTGTCGCTGCTGCTGCCCCAAGGCCTTCCTGTCCCGCGGGAAGCGG
CAGGAGCCGCCGCCGACACCTGAAGGAAAATTGGGCCGATTTCCACCTATGATGCATCATCA
CCAGGCACCCTCAGATGGCCAGACTCCTGGGGCTCGTTTCCAGAGGTCTCACCTTGCCGAGG
CATTTGCAAAGGCCAAAGGATCAGGTGGAGGTGCTGGAGGAGGAGGTAGTGGAAGAGGTCTG
ATGGGGCAGATTATTCCAATCTACGGTTTTTGGGATTTTTTTATATATACTGTACATTCTATT
TAAGGTAAGTAGAATCATCCTAATCATATTACATCAATGAAAAATCTAATATGGCGATAAAAA
TCATTGTCTACATTAAACTTCTTATAGTTCATAAAATTATTTCAAATCCATCATCTCTTTA
AATCCTGCCTCCTCTTCATGAGGTACTTAGGATAGCCATTATTTCAAGTTTCACATAAGAATG
TTTACTCAATGTTTAAGTGTTTTGCCCCAAAATTCACTAACAAGGCAGAACTAGGACTT
GAACATGGATCTTTTGGTCTTAATCCAGTGAGTGATACAATTCAATGCACTCCCCTGCCA

009111.11101

FIGURE 302

MAYSTVQRVALASGLVLALSLLLPKAFLSRGKRQEPPTPEGKLGRFPPMMHHHQAPSDGQT
PGARFQRSHLAEAFKAKGSGGGAGGGGSGRGLMGQIIPYGFIFLYILYILFKVSRIILI
ILHQ

00011314151617181920

FIGURE 303

CGGCTCGAGTGCAGCTGTGGGGAGATTTCAGTGCATTGCCTCCCCTGGGTGCTCTTCATCTT
GGATTTGAAAGTTGAGAGCAGCATGTTTTGCCCACTGAAACTCATCTGCTGCCAGTGTAC
TGGATTATTCCTTGGGCTGAATGACTTGAATGTTTCCCGCCTGAGCTAACAGTCCATGTG
GGTGATTGAGCTCTGATGGGATGTGTTTCCAGAGCACAGAAGACAAATGTATATTCAAGAT
AGACTGGACTCTGTCAAGGAGAGCACGCCAAGGACGAATATGTGCTATACTATTACTCCA
ATCTCAGTGTGCCTATTGGGCGCTTCCAGAACCGGTACACTTGATGGGGGACATCTTATGC
AATGATGGCTCTCTCTGCTCCAAGATGTGCAAGAGGCTGACCAGGGAACCTATATCTGTGA
AATCCGCTCAAAGGGGAGAGCCAGGTGTTCAAGAAGGCGGTGGTACTGCATGTGCTTCCAG
AGGAGCCCAAAGAGCTCATGGTCCATGTGGTGGATTGATTGAGATGGGATGTGTTTTCCAG
AGCACAGAAGTAAACACGTGACCAAGGTAGAATGGATATTTTCAGGACGGCGCGCAAAGGA
GGAGATTGTATTTCTGTACTACCAAACTCAGGATGTCTGTGGAGTACTCCAGAGCTGGG
GCCACTTCCAGAATCGTGTGAACCTGGTGGGGACATTTCCGCAATGACGGTCCATCATG
CTTCAAGGAGTGAGGGAGTCAGATGGAGGAAACTACACTGCAGTATCCACCTAGGGAACCT
GGTGTTCAGAAACCATTTGTGCTGCATGTCAGCCCGGAAGACCTCGAACACTGGTGACCC
CGGCAGCCCTGAGGCCTCTGGTCTTGGGTGGTAATCAGTTGGTGATCATTGTGGGAATTGTC
TGTGCCACAATCCTGCTGCTCCCTGTTCTGATATTGATCGTGAAGAAGACCTGTGGAAATAA
GAGTTCAGTGAATCTACAGTCTTGGTGAAGAACAGGAAGACTAATCCAGAGATAAAAG
AAAAACCTGCCATTTTGAAGATGTGAAGGGGAGAAACACATTTACTCCCCAATAATTGTA
CGGGAGGTGATCGAGGAAGAAGAACCAAGTGAAAAATCAGAGGCCACCTACATGACCATGCA
CCCAGTTTGGCCTTCTCTGAGGTCAGATCGGAACAACCTCACTTGAAAAAAGTCAGGTGGGG
GAATGCCAAAAACACAGCAAGCCTTTTGAAGAATGGAGAGTCCCTTCATCTCAGCAGCGG
TGGAGACTCTCTCCTGTGTGTCTCTGGGCCACTCTACCAGTGATTTCAGACTCCCCTCTC
CCAGCTGTCTCTCTGCTCATTGTTTGGTCAATACACTGAAGATGGAGAATTTGGAGCCTGG
CAGAGAGACTGGACAGCTCTGGAGGAACAGGCCCTGCTGAGGGGAGGGGAGCATGGACTTGGC
CTCTGGAGTGGGACACTGGCCCTGGGAACAGGCTGAGCTGAGTGCCCTCAAACCCCCGTT
GGATCAGACCCTCCTGTGGGCGAGGTTCTTAGTGGATGAGTACTGGGAAGAATCAGAGATA
AAAACCAACCCAAATCAA

MFCPLKLILLPVLLDYSGLGNDLNVSPPELTVHVGDSSALMGCVFQSTEDKCIFKIDWTLSPG
EHAKDEYVLYYNSLVPIGRFQNRVHLMGDILCNDGSLLLQDVQEAADQGTYYICEIRLKGES
QVFKKAVLVHLVPEEPKELMVHVGGILQMGCVFQSTEVKHVTVKEWTFSGRRAKEEIVFRYY
HKLMSVEYSQSWGHFQNRVNLVGDIFRNDGSI MLQGVRES DGGNYTCSIHLGNLVFKKTI V
LHVSPEEPRTLVTPAALRPLRGGNQLVLIIVGIVCATILLPLVILIVKKT CGNKSSVNST
LVNKT KTKNPEIKEKPKFCEBGEKHIYSPIIVREVIEEEPESEKSEATYMTMHVPWPSLR
SDRNSLEKKSGGGMPKTOOAF

FIGURE 305

CTATGAAGAAGCTTCCTGGAAAACAATAAGCAAAGGAAAACAAATGTGTCCCATCTCACATG
 GTTCTACCCCTACTAAAGACAGGAAGATCATAAACTGACAGATACTGAAATTGTAAGAGTTGG
 AAACACATTTTGCAAAGTCATTGAACTCTGAGCTCAGTTGCAGTACTCGGGAAGCC**ATG**CA
 GGATGAAGATGGATACATCACCTTAAATATTA~~AA~~AACTCGGAAACCAGCTCTCGTCTCCGTTG
 GCCCTGCATCCTCCTCCTGGTGGCGTGTGATGGCTTTGATTCTGCTGATCCTGTGCGTGGGG
 ATGGTTGTGCGGGCTGGTGGCTCTGGGGATTTGGTCTGTCATGCAGCGCAATTACCTACAAGA
 TGAGAATGAAAATCGCACAGGAACTCTGCAACAATTAGCAAAGCGCTTCTGTCAATATGTGG
 TAAAACAATCAGAACTAAAGGGCACTTTC~~AA~~AGGTCA~~AA~~ATGCAGCCCCGTGACACAAAC
 TGGAGATATTATGGAGATAGCTGCTATGGGTTCTTCAGGCACAACCTAACATGGGAAGAGAG
 TAAGCAGTACTGCACTGACATGAATGCTACTCTCCTGAAGATTGACAACCGGAACATTGTGG
 AGTACATCAAAGCCAGGACTCATTTAATTCGTTGGGTCGGATTATCTCGCCAGAAGTCGAAT
 GAGGTCTGGAAGTGGGAGGATGGCTCGGTTATCTCAGAAAATATGTTTGAGTTTTTGGGAAGA
 TGGAAAAGGAAATATGAATTGTGCTTATTTTCATAATGGGAAAATGCACCTACCTTCTGTG
 AGAACAAACATTATTTAATGTGTGAGAGGAAGGCTGGCATGACCAAGGTGGACCAACTACCT
TAATGCAAAGAGGTGGACAGGATAACACAGATAAGGGCTTTATTGTACAATAAAAGATATGT
 ATGAATGCATCAGTAGCTGAAAAAAAAAAAAA

099181-11601

FIGURE 306

MQDEGDYITLNIKTRKPALVSVGPASSSWRVMALILLILCVGMVVGLVALGIWSVMQRNYL
QDENENRTGTLLQQLAKRFQYVVKQSELKGTFKGHKSCPCDNTWRYYGDSCYGFFRHNLTWE
ESKQYCTDMNATLLKIDNRNIVEYIKARTHLIRVWGLSRQKSNEVWKWEDGSVISENMFEFL
EDGKGNMNCAYFHNGKMHPTFCENKHYLMCERKAGMTKVDQLP

FIGURE 307

CCCACGCGTCCGCGCAGTCGCGCAGTTCTGCCTCCGCCTGCCAGTCTCGCCCGGATCCCGG
 CCGGGGGCTGTGGCGTCGACTCCGACCCAGGCAGCCAGCAGCCGCGCGGGAGCCGGACCGC
 CGCCGGAGGAGCTCGGACGGCATGCTGAGCCCCCTCCTTTGCTGAAGCCGAGTGCGGAGAA
 GCCCCGGCAAACGCAGGCTAAGGAGACCAAAGCGGCGAAGTCGCGAGACAGCGGACAAGCAG
 CGGAGGAGAAGGAGGAGGAGGCGAACCAGAGAGGGGCAGCAAAAGAAGCGGTGGTGGTGGG
 CGTCGTGGCCATGGCGGCGGCTATCGCCAGCTCGCTCATCCGTCAGAAGAGGCAAGCCCGCG
 AGCGCGAGAAATCCAACGCCTGCAAGTGTGTCAGCAGCCCCAGCAAAGGCAAGACCAGCTGC
 GACAAAAACAAGTTAAATGTCTTTTCCGGGTCAAACCTCTTCGGCTCCAAGAAGAGGCGCAG
 AAGAAGACCAGAGCCTCAGCTTAAGGGTATAGTTACCAAGCTATACAGCCGACAAGGCTACC
 ACTTGCAGCTGCAGGCGGATGGAACCATGTGATGGCACCAGATGAGGACAGCACTTACACT
 CTGTTTAACCTCATCCCTGTGGGTCTGCGAGTGGTGGCTATCCAAGGAGTTCAAACCAAGCT
 GTACTTGGCAATGAACAGTGAGGGATACTTGTACACCTCGGAACTTTTACACCTGAGTGCA
 AATTCAAAGAATCAGTGTTTGAATAATTATGTGACATATTCATCAATGATATACCGTCAG
 CAGCAGTCAGGCCGAGGGTGGTATCTGGGTCTGAACAAAGAAGGAGAGATCATGAAAGGCAA
 CCATGTGAAGAAGAACAAGCCTGCAGCTCATTTTCTGCCTAAACCACTGAAAGTGGCCATGT
 ACAAGGAGCCATCACTGCACGATCTCACGGAGTCTCCCGATCTGGAAGCGGGACCCCAACC
 AAGAGCAGAAGTGTCTCTGGCGTGCTGAACGGAGGCAAATCCATGAGCCACAATGAATCAAC
GTAGCCAGTGAGGGCAAAAGAAGGGCTCTGTAACAGAACCTTACCTCCAGGTGCTGTTGAAT
 TCTTCTAGCAGTCCTTACCCAAAAGTTCAAATTTGTCAGTGACATTTACCAAACAACAGG
 CAGAGTTCATACTTCTATCTGCCATTAGACCTTCTTATCATCCATACTAAAGC

FIGURE 308

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA28498
><subunit 1 of 1, 245 aa, 1 stop
><MW: 27564, pI: 10.18, NX(S/T): 1
MAAAIASSLIRQKRQAREREKSNACKCVSSPSKGKTSCDKNKLNVFSRVKLFSGSKKRRRRRP
EPQLKGIVTKLYSRQGYHLQLQADGTIDGTDKEDSTYTLFNLIPVGLRVVAIQGVQTKLYLA
MNSEGILYTSELFTPECKFKESVFENYYVTYSSMIYRQQQSGRGWYLGLENKEGEIMKGNHVK
KNKPAAHFLPKPLKVAMYKEPSLHDLTEFSRSGSGTPTKRSRSVSGVLNGGKSMHNEST

N-glycosylation site.

amino acids 242-246

Glycosaminoglycan attachment site.

amino acids 165-169, 218-222

Tyrosine kinase phosphorylation site.

amino acids 93-100

N-myristoylation site.

amino acids 87-93, 231-237

ATP/GTP-binding site motif A (P-loop).

amino acids 231-239

HBGF/FGF family proteins

amino acids 78-94, 102-153

FIGURE 309

CCAGGATGGAGCTGGGGCCTGTATAGCCATATTATTGTTCTATGCTACTAGACATGGGGGGG
 ACTTGGTGAAAAAGGTATTATCCAGCCAGAGGGTCTGGGAGCCCTGTCCTACTGAACCTGGG
 CAACCTGGATATTCTGAGACATATTTTGGGGGGATTTCAGTGAAAAAGTGGGGGATCCCTT
 CCATTTAGAGTGTAGCAAAGGAAAAAACACCAAGGTTGGGTTCCCTTCTGACATTGGCAGTG
 CCCAGTAGGGGTGGGATGAGCGAATATTCCAAAGCTAAAGTCCACACCTGTAGATTAC
 AAGAGTGGATTTTGGCAGGAGTGTGCCCCAAAATACAGTGGAAAGGTGCCTGAAGATATTTAA
 ACCACGCTCTGGAAATTTAGTGGGTCTTGGCTTTGGGATAGGTGAAGTGAGGACAGACACTG
 GAGAGGAGGGAAAGGGGACGTTTTCAATAGGAGGCAAACTCGAGGGTGGGATCCACTGAGG
 AGTACATAGGCTGCTGGATCTGGTGGAGCCAGCACTGGGCCCACGGGTGGTAAGTGGCTGCT
 GTGGAGGGGGGTACGTGAGGGGGGGGTCTGGGGCTTATCCTCAGTCTCTGTGGGTGGGGCAG
 CGAGTCGGGGCCTGAGCGTCAAGAGCATGCCCTAGTGAGCGGGCTCCTCTGGGGGAGCCAG
 CGCGCTCCGGGCGCCTGCCGGTTTGGGGGTGTCTCCTCCCGGGGCGCTATGCGCGCGCTGGC
 CAGTAGCCTGATCCGCGAGAAGCGGGAGGTCCGCGAGCCCGGGGGCAGCCGGCCGCTGTGCG
 CGCAGCGCGCGTGTGTCCCCGCGGCACCAAGTCCCTTTGCCAGAAGCAGCTCCTCATCCTG
 CTGTCCAAGGTGCGACTGTGCGGGGGGCGGCCGCGCGGCCGACCGCGGCCCGGAGCCTCA
 GCTCAAAGGCATCGTCACCAAACTGTTCTGCGCCAGGGTTTCTACCTCCAGGCGAATCCCG
 ACGGAAGCATCCAGGGCACCCAGAGGATACAGCTCCTTCACCCACTTCAACCTGATCCCT
 GTGGGCTCCGTGTGGTCACCATCCAGAGCGCCAAGCTGGGTCACTACATGGCCATGAATGC
 TGAGGAGCTGCTCTACAGTTCCCGCATTTTACAGCTGAGTGTGCGCTTAAAGGAGTGTGTCT
 TTGAGAATTACTACGTCTGTACGCCTCTGCTCTCTACCGCCAGCGTCTGTCTGCGCGGGCC
 TGGTACCTCGGCCTGGACAAGGAGGGCCAGGTCATGAAGGAAACCGAGTTAAGAAGACCAA
 GGCAGCTGCCACTTTCTGCCAAGCTCCTGGAGGTGGCCATGTACCAGGAGCCTTCTCTCC
 ACAGTGTCCCGAGGCCTCCCTTCCAGTCCCCCTGCCCTTGAATGTAGTCCCTGGACTG
 GAGGTTCCCTGCACTCCAGTGAGCCAGCCACCACCAACCTGT

FIGURE 310

MAALASSLIRQKREVREPGGSRPVSAQRRVCPRGTKSLCQKQLLILLSKVRLCGGRPARPDR
GPEPQLKGIVTKLFCRQGFYLANPDGSIQGTPEDTSSFTHFNLI PVGLRVVTIQSAKLGHY
MAMNAEGLLYSSPHFTAECRFKECVFENYYVLYASALYRQRSGRAWYLGLDKEGQVMKGNR
VKKTAAAHLPLKLEVAMYQEPSLHSVPEASPSPPAP

Tyrosine kinase phosphorylation site:

amino acids 199-207

N-myristoylation sites:

amino acids 54-60, 89-95, 131-137

HGF/FGF family signature:

amino acids 131-155

FIGURE 311

ATGCGCCGCGGCCATCGTAGCGGCTTGATCCGCCAGAAGCGGCAGGCGGGGAGCAGCACTG
GGACCGGCGCTGTGCCAGCAGGAGGCGGAGCAGCCCCAGCAAGAACCGGGGCTCTGCAACG
GCAACCTGGTGGATATCTTCTCCAAAGTGCGCATCTTCGGCCTCAAGAAGCGCAGTTGCGG
CGCCAAGATCCCCAGCTCAAGGTTATAGTGACCAGGTTATATGTCAGGCAAGGCTACTACTT
GCAATGCACCCCGATGGAGTCTCGATGGAACCAAGGATGACAGCACTAATTCTACACTCT
TCAACCTCATACCACTGGGACTACGTGTTGTTGCCATCCAGGGAGTAAAAACAGGGTTGTAT
ATAGCCATGAATGGAGAAGGTTACCTCTACCCATCAGAACTTTTACCCCTGAATGCAAGTT
TAAAGAATCTGTTTTTAAAAATTATTATGTAATCTACTCATCCATGTTGTACAGACAACAGG
AATCTGGTAGAGCCTGGTTTTTGGGATTAATAAGGAAGGCGAAGTATGAAGAGGAACAGA
GTAAAGAAAAACCAACAGCAGCTCATTTTCTACCGAAGCCATTGGAAGTTGCCATGTACCG
AGAACCATCTTTGCATGATGTTGGGGAACAGGTCCCGAAGCCTGGGGTGACGCCAAGTAAAA
GCACAAAGTGCCTCGCAATAATGAATGGAGGCAAAACAGTCAACAAGAGTAAGACAACATAG

FIGURE 312

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA28503

><subunit 1 of 1, 247 aa, 1 stop

><MW: 27702, pI: 10.36, NX(S/T): 2

MAAAIASGLIRQKRQAREQHWDPRPSASRRSSPSKNRGLCNGNLVDIFSKVRI FGLKKRRRLR
RQDPQLKGIVTRLYCRQGYLLQMHPDGDALDGTKDDSTNSTLFNLI PVGLRVVAIQGVKTGLY
IAMNGEGYLYPSELFTECKFKESVFENYYVIYSSMLYRQQESGRAWFLGLNKEGQAMKGNR
VKKTKPAAHFLPKPLEVAMYREPSLHDVGETVPKPGVTPSKSTSASAIMNGGKPVNKSSTT

N-glycosylation site.

amino acids 100-104, 242-246

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 28-32, 29-33

Tyrosine kinase phosphorylation site.

amino acids 199-207

N-myristoylation site.

amino acids 38-44, 89-95, 118-124, 122-128, 222-228

HBCF/FGF family proteins.

amino acids 104-155, 171-198

FIGURE 313

GGGGAGAGGAATTGACCATTGATAAAAGGAGACTTTTTTTTTTGGTGGTGGTGGCTGTGGGTGCCTTGCAAAAAAT
 GAAGGATGCAGGACGCAGCTTTCTCCTGGAACCGAACGCAATGGATAAACTGATTGTGCAAGAGAGAAGGAAGA
 ACGAAGCTTTTTCTGTGAGCCCTGGATCTTAACACAAATGTGTATATGTGCACACAGGAGCATTCAAGAAATG
 AAATAAACAGAGTTAGACCCCGCGGGGTGGTGTCTTGACATAAATAAATAATCTTAAAGCAGCTGTTCC
 CTCACCCACCCCAAAAAAAGGATGATTGGAATGAAGAACCAGGATTCACAAAGAAAAAGTATGTTCAATT
 TTCTCTATAAAGGAGAAAGTGAGCCAAGGAGATATTTTGGAAATGAAAGTTTGGGGCTTTTTAGTAAAGTAA
 AGAAGCTGGTGTGGTGGTGTCTTCTTCTTTTGAATTTCCCACAAGAGGAGAGAAATTAATAATACATCTGC
 AAGAAATTTAGAGAGAAGAAAGTTGACCGCGGCAGATTGAGGCATTGATTGGGGAGAGAAACACGAGAGCA
 CAGTTGGATTTGTGCCTATTGTTGACTAAATTTGACGGATAATTCAGTTGGATTTTCTTCATCAACCTCCTTT
 TTTTTAAATTTTTATTCTTTTGGTATCAAGATCATGCGTTTTCTCTGTTCTTAACACACCTGGATTTCCATCT
 GGATGTTGCTGTGATCAGTCTGAATACAACCTGTTGAATTCAGAAGGACCAACACAGATAAATATGATG
 TTGAACAAGATGACCTTACATCCACAGCAGATAATGATAGTCTAGGTTTAAACAGGCCCCATTGACCCCCCT
 GCTGTGTGGTGTGCTGGCTCTTCACTTCTTGTGGTGGCTGGTCTGGTGGGGCTCAGACCTGCCCTTCTGTGT
 GCTCCTGCAGCAACAGCTTCAGCAAGGTGATTGTGTTCGGAACCTGGCTGAGGTTCCGGATGGCATCTCC
 ACCAACACACCGGCTGCTGAACCTCCATGAGAACCATAATCCAGATCATCAAAGTGAACAGCTTCAAGCATTTGAG
 GCACCTTGGAAATCTACAGTTGAGTAGGAACCATATCAGAACCATTGAAATTTGGGGCTTTCAATGGTCTGGCGA
 ACCTCAACACTCTGGAACCTTTGACAAATCGTCTTACTACCATCCGAATGGAGCTTTGTATACTTGTCTAAA
 CTGAAGGAGCTCTGGTTGCGAAACACCCCATGAAAGCATCCCTTCTTATGCTTTTAAACAGAATTCCTCTCTT
 GCGCCGACTAGACTTAGGGGAATGAAAGACTTTTATACATCTCAGAAGGTGCCTTTGAAGGTCTGTCCAAT
 TGAGGTATTGAACTTGGCACTTGCAACCTTCGGGAATCCCTAACCTCACACCGCTCATAAACTAGATGAG
 CTGGATCTTTCTGGGAATCATTTATCTGCCATCAGGCTGGCTCTTCCAGGGTTTGATGCACCTTCAAAAACT
 GTGGATGATACAGTCCAGATTCAAGTGATTGAACGGAATGCCTTTGACAACCTTCAGTCACTAGTGGAGATCA
 ACCTGGCACACAATAATCTAACATTACTGCCTCATGACCTCTTCACTCCCTTGCATCATCTAGACGGATACAT
 TTACATCAACAACCTTGGAACTGTAAGTGTGACATCTGTGGCTCAGCTGGTGGGATAAAGACATGGCCCCCTC
 GAACACAGCTTGTGTGCCCCGGTGAACACTCCTCCCAATCTAAAGGGGAGGTACATTGGAGAGCTCGACCAGA
 ATTACTTCACATGCTATGCTCGGGTATTGTGGAGCCCCCTGCAGACCTCAATGTCACTGAAGGATGGCAGCT
 GAGCTGAAATGTCGGGGCTCCACATCCCTGACATCTGTATCTTGGATTACTCCAAATGGAACAGTCATGACACA
 TGGGGCGTACAAGTGGCGATAGCTGTGCTCAGTGATGGTACGTTAAATTTACAAATGTAACTGTGCAAGATA
 CAGGCATGTACACATGTATGGTGAATAATCCGTTGGGAATACTACTGCTTCAGCCACCTGAATGTTACTGCA
 GCAACCACTACTCCTTTCTTACTTTTCAACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCAG
 GACCACAGATAACAATGTGGGTCCCACTCCAGTGGTGCAGCTGGGAGACCAACATGTGACCACCTCTCTCACAC
 CACAGAGCACAAGGTGCAGAGAGAAAACTTCACCATCCAGTGACTGATATAAACAGTGGGATCCAGGAAT
 GATGAGGTGATGAAGACTACCAAAATCATATTGGGTGTTTTGTGGCCATCACACTCATGGCTGCAGTGATGCT
 GGTCAATTTCTACAAGATGAGGAAGCAGCCATCGGCAAAACCATCACGCCCCAACAGGACTGTTGAAATTA
 TTAATGTGGATGATGAGATTACGGGAGACACACCATGGAAGCCACCTGCCATGCTGCTATCGAGCATGAG
 CACCTAAATCACTATAACTCATACAAATCTCCCTTCAACCACACAACAAGTAAACACAATAAATCAATACA
 CAGTTGAGTGCATGAACGTTATTGATCCGAATGAACCTTAAAGACAATGTACAGAGACTCAAACTCAAAACA
 TTTACAGAGTTACAAAAACAAACAAATCAAAAAAAGACAGTTTATTAATAATGACACAATGACTGGGCTAA
 ATCTACTGTTTCAAAAAGTGTCTTTACAAAAAACAAAAAGAAAGAAATTTATTTATTAATAATCTATTG
 TGATCTAAAGCAGACAAAA

FIGURE 314

MLNKMTLHPQQIMIGPRFNRLFDPLLVLALLQLLVVAGLVRAQTCPSVCSCSNQFSKVIC
 VRKNLREVPDGISTNTRLNLHENQIQIIVKNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA
 NLNTLELFDNRLTTPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLS
 YISEGAFEGLSNRLYNLAMCNLREIPNLTPLIKLDELDSLGNHLSAIRPGSFQGLMHLQKL
 WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLLHNPWNCNDIL
 WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAE
 LKCRASSTLSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVDQDGMVTCMVSNSVGN
 TTASATLNVTAATTPFSYFSTVTVETMEPSQDEARTTDNNVGPTFVVDWETTNVTTSLTPQ
 STRSTEKTFITPVDINSIGIPGIDEVMKTKIIIGCFVAITLMAAVMLVIFYKMRKQHRQN
 HHAPTRTVEIINVDEITGDTFMESHLPMPAIEHEHLNHYSYKSPFNHTTTVNTINSIHSS
 VHEPLLIRMNSKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419,
 434-438, 442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
 391-397, 422-428, 433-439, 531-537

FIGURE 315

GCGCCGGGAGCCCATCTGCCCCAGGGGCACGGGGCGCGGGGCCGGCTCCCGCCCGGCACAT
 GGCTGCAGCCACCTCGCGCGCACCCCCAGGCGCCGCGCCAGCTCGCCCGAGGTCGGTCGGA
 GCGCGCCGGCGCCCCGGAGCCAAAGCAGCAACTGAGCGGGGAAGCGCCCCGCTCCGGGGATC
 GGG**ATG**TCCTCCTCTTCTCTCTTGCTAGTTTCTACTATGTTGGAACCTTGGGGACTCA
 CACTGAGATCAAGAGAGTGGCAGAGGAAAAGGTCACTTTGCCCTGCCACCATCAACTGGGGC
 TTCAGAAAAAGACACTCTGGATATTGAATGGCTGCTCACCGATAATGAAGGGAACCAAAAA
 GTGGTGATCACTTACTCCAGTCGTCATGTCTACAATAACTTGACTGAGGAACAGAAGGCCG
 AGTGGCCTTTGCTTCCAATTTCTGGCAGGAGATGCCTCCTTGCAAGTTGAACCTCTGAAGC
 CCAGTGATGAGGGCCGGTACACCTGTAAGGTTAAGAAATCAGGGCGCTACGTGTGGAGCCAT
 GTCATCTTAAAAAGTCTTAGTGAGACCATCCAAGCCCAAGTGTGAGTTGGAAGGAGAGCTGAC
 AGAAGGAAGTGACCTGACTTTGCAGTGTGAGTCATCCTCTGGCACAGAGCCCATTTGTGTATT
 ACTGGCAGCGAATCCGAGAGAAAGAGGGAGAGGATGAACGTCTGCCTCCCAAATCTAGGATT
 GACTACAACCACCCTGGACGAGTTCTGCTGCAGAATCTTACCATGTCTACTCTGGACTGTA
 CCAGTGCACAGCAGGCAACGAAGCTGGGAAGGAAAGCTGTGTGGTGCGAGTAAGTGTACAGT
 ATGTTACAAGCATCGGCATGGTTGCAGGAGCAGTGACAGGCATGTGGCTGGAGCCCTGCTG
 ATTTTCTCTTGTTGGCTGCTAATCCGAAGGAAAGACAAGAAAGATATGAGGAAGAAGA
 GAGACCTAATGAATTCGAGAAGATGCTGAAGCTCCAAAAGCCCGTCTTGTGAACCCAGCT
 CCTCTTCTCAGGCTCTCGGAGCTCACGCTCTGGTTCTTCTCCACTCGCTCCACAGCAAT
 AGTGCCTCACGCAGCCAGCGGACACTGTCAACTGACGCAGCACCCAGCCAGGGCTGGCCAC
 CCAGGCATACAGCCTAGTGGGGCCAGAGGTGAGAGGTTCTGAACCAAGAAAGTCCACCATG
 CTAATCTGACCAAGCAGAAACCACACCAGCATGATCCCGAGCCAGAGCAGAGCCTTCCAA
 ACGGTCT**TGA**ATTACAATTGGACTTGACTCCCACGCTTCTTAGGAGTGAGGGTCTTTGGACTC
 TTCTCGTCAATTGGAGCTCAAGTCACAGCCACACAACCATGAGAGGTCACTAAGTAGCA
 GTGAGCATTGCACGGAACAGATTAGATGAGCATTTTCTTATACAAATACCAACACAGCAAA
 AGGATGTAAGCTGATTCATCTGTAAAAAGGCATCTTATTGTGCCTTTAGACCAGAGTAAGGG
 AAAGCAGGAGTCCAAATCTAATTTGTTGACCAGGACCTGTGGTGAGAAGGTTGGGGAAGGTG
 AGGTGAATATACCTAAAACCTTTAATGTGGGATATTTGTATCAGTGCTTTGATTACAATTT
 TCAAGAGGAAATGGGATGCTGTTGTAAATTTCTATGCATTTCTGCAAACTTATTGGATT
 ATTAGTTATTAGACAGTCAAGCAGAACCCACAGCCTTATTACACCTGTCTACACCATGTAC
 TGAGCTAACCACTTCTAAGAACTCCAAAAAGGAACATGTGTCTTCTATTCTGACTTAAC
 TTCATTGTGCATAAGGTTTGGATATTAATTTCAAGGGGAGTTGAAATAGTGGGAGATGGAGA
 AGAGTGAATGAGTTTCTCCCCTCTATACTAATCTCACTATTTGTATTTGAGCCCAAAATAAC
 TATGAAGAGGAGACAAAAATTTGTGACAAAGGATTGTGAAGAGCTTTCATCTTCATGATGTT
 ATGAGGATTGTTGACAAACATTAGAAATATATAATGGAGCAATTTGGGATTTCCTCAAT
 CAGATGCGCTCTAAGGACTTTCTGCTAGATATTTCTGGAAGGAGAAATACAAATGTCTATT
 TATCAACGTCCTTAGAAGAATTTCTTCTAGAGAAAAGGGATAGGAATGCTGAGAAATGCTGAAAGATT
 CCCAACATACCATATAGTCTCTCTTTCTGAGAAAAATGTGAACAGAAATGCAAGACATGG
 GTGGACTAGAAAAGGAGATTAGATCAGTTTCTCTTAATATGTCAAGGAAGGTAGCCGGGCA
 TGGTGCCAGCCCTGTAGGAAAAATCCAGCAGGTGGAGGTTGCAGTGAGCCGAGATTATGCC
 ATTGCACTCCAGCCTGGGTGACAGAGCGGACTCCGCTCTC

FIGURE 316

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45419

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41281, pI: 8.33, NX(S/T): 3

MSLLLLLLLLVSYVGTGLGTHTEIKRVAEEKVTLPCHHQLGLPEKDTLDIEWLLTDNEGNQKV
VITYSSRHVYNNLTTEEQGRVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSGRYVWSHV
ILKVLVRPSKPKCELEGELTEGSDLTLCESSSGTEPIVYYWQRIREKEGEDERLPPKSRID
YNHPGRVLLQNLMTMSYSGLYQCTAGNEAGKESCVVRVTQYVQSIGMVAGAVTGIVAGALLI
FLLVWLLIRRKDKERYEEEEERPNEIREDAEAPKARLVKPSSSSSGSRSSRSRSGSSSTRSTANS
ASRSQRTLSTDAAPQPLATQAYSLVGPEVRGSEPKKVHHANLTKAETTPSMIPSQSRAFQTV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 232-251

FIGURE 317

CGCGAGGCGCGGGGAGCCTGGGACCAGGAGCGAGGCCCTACCTGCAGCCGCCGCCACGGCAGCGCAGCCA
 CCATGCGCGCTCTGCTGTGCTCTGCTGCTCTGTCGCGAGTAGTGGAATTCGCGCAGAAAGTTTGAGTATCACTACT
 CCTGAAGAGATGATTGAAAAGGCCAAAGGGAAACTGCCATCTGCCATGCAAAATTTACGCTTAGTCCCGAAGA
 CCAGGAGCCGCTGGACATCGAGTGGCTGATATCACCAGCTGATAATCAGAAGGTGGATCAAGTGATTATTTAT
 ATTTCTGGAGACAAAATTTATGATGACTACTATCCAGATCTGAAAGGCCGAGTACATTTTACGAGTAATGATCTC
 AAATCTCGTGATGATCAATAAATGTAAACGAATTTACAACCTGTCAGATATTGGCCATATTCAGTGCAAAGTCTC
 AAAAGCTCTCGTGTGTTCCAAATAAGAGATTTCATCTGCTAGTCTTCTGTTAAGCCTTCAGTGCAGAGTGTTACG
 TTGATGGATCTGAAGAAATTTGGAAGTGACTTTAAGATAAAATGTGAACCAAAAGAGGTTCACTTCCATTACAG
 TATGAGTGGCRAAAATTTGCTGACTCACAGAAATGCCACTTCATGGTTAGCAGAAATGACTTCACTGTATT
 ATCTGTAAAAAATGCCCTCTCTGAGTACTCTGGACATACAGCTGTACAGTCAAAAACAGAGTGGCGCTCTGATC
 AGTGCCCTGTTGCGCTCAAAAGCTTGCCTCCTTCAAAATAAAGCTGGACTAAATTCAGAGGCCATTATAGGAACT
 TTGCTTGCTCTAGCGCTCATTTGGTCTTATCATCTTTTGTCTGCTGTAAGAGCGCAGAGAGAAAATATGAAA
 GGAAGTTTATCACGATATCAGGGAAGATGTGCCACCTCCAAGAGCCGTCAGTCCACTGCCAGAGCTAGATCG
 GCAGTAATCATTCATCCCTGGGGCCATGTCTCCTTCCAACATGGAAGGATATCCAGACTCAGTATAACCAA
 GTACCAAGTGAAGACTTTGAACGCACCTCTCAGATCCGACTCTCCCACCTGCTAAGTTCAAGTACCCTTACAA
 GACTGATGGAATTACAGTTGTATTAATATGGACTACTGAAGATCTGAAGTATTGATTATTTGACTTTATTTT
 AGGCCTCTAGTAAAGACTTTAAATGTTTTTAAAAAAGCACAAGGCACAGAGATTAGAGCAGCTGAAGAACAC
 ATCTACTTTATGCAATGGCATTAGACATGTAAGTCAGATGTCATGTCAAAATTAGTACGAGCCAAATTCCTTTGT
 TAAAAAACCTTATGTATAGTGACACTGATAGTTAAAGATGTTTTATTATATTTCAATAACTACCCTAACAA
 ATTTTTAACTTTTCAATATGCATATTCTGATATGTGGTCTTTTAGGAAAAGTATGGTTAAATAGTTGATTTTCAA
 AGGAAATTTTAAATCTTACGTTCTGTTAATGTTTTTGTATTTAGTTAAATACATTGAAGGGAAATACCCG
 TTTCTTTCCCTTTTATGCACACAACAGAAACAGCGCTTGTCATGCCTCAAACATTTTTTTATTTGCAACTACA
 TGATTTTACACAATTTCTCTTAAACACGACATAAAATAGATTTCCTTGATATAAATACTTACATACGCTCCA
 TAAAGTAAATTTCTCAAAGGTGCTAGAACAATCGTCCACTTCTACAGTGTCTCGTATCCAACAGAGTTGATGC
 ACAATATATAAATACTCAAGTCCAATATTAACAACTTAGGCACCTGACTTAACTTTATAAAAAATTTCTCAAACFA
 TATCAATATCTAAAGTGCATATATTTTTAAGAAAGATTATCTCAATAACTTCTATAAAAAATAAGTTTGATGG
 TTTGGCCCATCTAACTTCACTACTATTTAGTAAAGACTTTTAACTTTTAAATGTGTAGTAGAGGTTTATTTCTACCTT
 TTTTCAACATGACACCAACACAATCAAAAACGAAGTTAGTGAGGTGCTAACTATGTGAGGATTAAATCCAGTGAT
 TCGCGTCAAAATGATTCAGGAGGAGGTACCATGTCACTGGAATTTGGCGGATATGTTTTATTTTTTCTCCCT
 TGATTTGGATAACCAAAATGGAACAGGAGGAGGATAGTGATTCTGATGGCCATTCCCTCGATACATTTCTGGCTT
 TTTTCTGGGCAAGGTTGCCACATTTGGAAGAGGTGGAATATAAGTTCTGAAATCTGTAGGGAAGAGAACAT
 TAAGTTAATTTCAAAGGAAAAATCATCATCTATGTTCCAGATTCTCATTAAGACAAAGTACCACAACT
 GAGATCACATCTAAGTGACACTCCTATTGTCAAGTCTAATAACATTAACAACTCATGTATAGGGGTATAA
 TGTATACAGGTGACCAATGTTTTCTGAATGCATAAGAAATGAATAACTCAACACAGTACTTCTTAAACAA
 CTTCAACCAAAAAGACCAAAACATGGAACGAATGGAAGCTTTGAAGGACATGCTGTTTTAGTCCATGCTTT
 CCAAGCTGGCTAGAGCCAGGAGTCACTTGGAGGCTTTTAAATACAAAGATTTGAGCTGGAGGCCATTGCTTT
 AGCAAACTAATGCAGAAACAGAAATCAACTACCGCATGTTCTCATTAATAGTGGAGGTAAATGATAAGACT
 TATGAACCAAAAGGAAGAAACATAGACATTTGAGATCTATTGTAGAGGGGGGGTGGGAGGAGGAAAGGAGCA
 GAAAAGATAACTATTGATGCTGCCCTTCAACCTGGGTGATGAAATAATATGTACAAACAATCCCTGTGCACACA
 TGTTTACCTATGGAACAAACCTTCATGTATCCCTAAACCTAAATAAAAGTTAAAAA
 AA
 AAAAAAAAAAAAAAAAAAAAAAAAAA

0509181.11601

FIGURE 318

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA82361

><subunit 1 of 1, 352 aa, 1 stop

><MW: 38938, pI: 7.86, NX(S/T): 3

MALLLCFVLLCGVDFARSLSIITPEEMIEKAKGETAYLPCKFTLSPEDQGGLDIEWLISPA
DNQKVDQVIILYSGDKIYDDYYPDLKGRVHFTSNDLKSGDASINVTNLQLSDIGTYQCKVKK
APGVANKKIHLVVLVKPSGARYVDGSEEIGSDFKIKCEPKEGSLPLQYEWQKLSDSQKMPT
SWLAEMTSSVISVKNASSEYSGTYSCTVRNRVGSQCLLRNLNVVPPSNKAGLIAGAIIGTLL
ALALIGLIIFCCRKKRREEKYKEVHHDIREDVPPPKSRTSTARSYIGSNHSSLGSMSPSNM
EGYSKTQYNQVPSDFERTPQSPTLPPAKFKYPYKTDGITVV

Signal sequence.

amino acids 1-19

Transmembrane domain:

amino acids 236-257

N-glycosylation sites.

amino acids 106-110, 201-205, 298-302

Tyrosine kinase phosphorylation sites.

amino acids 31-39, 78-85, 262-270

N-myristoylation sites.

amino acids 116-122, 208-214, 219-225, 237-243, 241-247,
245-251, 296-302

Myelin P0 protein.

amino acids 96-125

FIGURE 319

TGAATGACTTCCACGGCTGGGACGGGAACCTTCCACCCACAGCTATGCCTCTGATTGGTGA
 ATGGTGAAGGTGCCTGTCTAACTTTTCTGTAAAAAGAACCAGCTGCCTCCAGGCAGCCAGCC
 CTCAAGCATCACTTACAGGACCAGAGGGACAAGACATGACTGTGATGAGGAGCTGCTTTCGC
 CAATTTAACACCAAGAAGAATTGAGGCTGCTTTGGGAGGAAGGCCAGGAGGAACACGAGACTG
 AGAGATGAATTTTCAACAGAGGCTGCAAGCCTGTGGACTTTAGCCAGACCCTTCTGCCCTC
 CTTTGCTGGCGACAGCCTCTCAAATGCAGATGGTTGTGCTCCCTTGCCCTGGGTTTTACCCTG
 CTTCTCTGGAGCCAGGTATCAGGGGCCAGGGCCAAGAATTCACCTTTGGGCCCTGCCAAGT
 GAAGGGGGTTGTTCCCCAGAACTGTGGGAAGCCTTCTGGGCTGTGAAAGACACTATGCAAG
 CTCAGGATAACATCACGAGTGCCCGGCTGCTGCAGCAGGAGGTTCTGCAGAACGTCTCGGAT
 GCTGAGAGCTGTTACCTTGTCACACCCTGCTGGAGTTCTACTTGAAAACCTGTTTTCAAAAA
 CCACCACAATAGAACAGTTGAAGTCAGGACTCTGAAGTCATTCTCTACTCTGGCCAACAAC
 TTGTTCTCATCGTGTCACTGCAACCCAGTCAAGAAAATGAGATGTTTTCCATCAGAGAC
 AGTGACACAGGCGGTTTTCTGCTATTCCGGAGAGCATTCAAACAGTTGGACGTAGAAGCAGC
 TCTGACCAAGCCCTTGGGGAAGTGGACATTCTTCTGACCTGGATGCAGAAATTCACAAGC
 TCTGAATGTCTAGACCAGGACCTCCCTCCCCCTGGCACTGGTTTGTCCCTGTGTCATTTCA
 AACAGTCTCCCTTCCTATGCTGTTCACTGGACACTTCACGCCCTTGCCCATGGGTCCCATTCT
 TTGGCCCAGGATTATTGTCAAAGAAGTCATTCTTTAAGCAGCGCCAGTGACAGTCAGGGAAG
 GTGCCTCTGGATGCTGTGAAGAGTCTACAGAGAAGATTCTTGATTTATTACAACCTATTTT
 AATTAATGTCAGTATTCAACTGAAGTTCTATTTATTTGTGAGACTGTAAGTTACATGAAGG
 CAGCAGAATATTGTGCCCCATGCTTCTTTACCCCTCACAATCCTTGCCACAGTGTGGGGCAG
 TGGATGGGTGCTTAGTAAGTACTTAATAAACTGTGGTGCTTTTTTTGGCCTGTCTTTGGATT
 GTTAAAAAACAGAGAGGATGCTTGGATGTAAAACCTGAACCTCAGAGCATGAAAATCACACT
 GTCTTCTGATATCTGCAGGGACAGAGCATTGGGGTGGGGGTAAGGTGCATCTGTTTGAAGG
 TAAACGATAAAATGTGGATTAAAGTGCCAGCACAAAGCAGATCCTCAATAAACATTTTCATT
 TCCCACCCACACTCGCCAGCTCACCCATCATCCCTTTCCTTGGTGCCCTCCTTTTTTTTTT
 TATCCTAGTCATTCTCCCTAATCTTCCACTTGAGTGTCAAGCTGACCTTGCTGATGGTGAC
 ATTGCACCTGGATGTACTATCCAATCTGTGATGACATCCCTGCTAATAAAAGACAACATAA
 CTCCAAAAA

320/330

FIGURE 320

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA88002

><subunit 1 of 1, 206 aa, 1 stop

><MW: 23799, pI: 9.12, NX(S/T): 3

MNFQQRLQSLWTLARPFPCPLLATASQMOMVVLPCLGFTLLLWSQVSGAQGGQEFHFGPCQVK
GVVPQKLWEAFWAVKDTMQAQDNITSARLLQQEVLQNVSDAESCYLVTILEFYLKTVFKNH
HNRTVEVRTLKSFSTLANNFVLIVSQLQPSQENEMFSIRDSAHRRFLLFRRAFKQLDVEAAL
TKALGEVDILLTWMQKFYKL

Signal sequence:

amino acids 1-42

N-glycosylation sites.

amino acids 85-89, 99-103, 126-130

FIGURE 321

AAGGAGCAGCCCGCAAGCACCAAGTGAGAGGC**ATG**AAGTTACAGTGTGTTTCCCTTTGGCTC
 CTGGGTACAATACTGATATTGTGCTCAGTAGACAACCACGGTCTCAGGAGATGTCTGATTTC
 CACAGACATGCACCATATAGAAGAGAGTTTCCAAGAAATCAAAGAGCCATCCAAGCTAAGG
 ACACCTTCCCAAAATGTCACTATCCTGTCCACATTGGAGACTCTGCAGATCATTAAAGCCCTTA
 GATGTGTGCTGCGTGACCAAGAACCTCCTGGCGTTCTACGTGGACAGGGTGTCAAGGATCA
 TCAGGAGCCAAACCCCAAAATCTTGAGAAAAATCAGCAGCATTGCCAACTCTTTCCTCTACA
 TGCAGAAAACCTCTGCGGCAATGTCAGGAACAGAGGCAGTGTCACTGCAGGCAGGAAGCCACC
 AATGCCACCAGAGTCATCCATGACAACTATGATCAGCTGGAGGTCCACGCTGCTGCCATTAA
 ATCCCTGGGAGAGCTCGACGTCTTCTAGCCTGGATTAATAAGAATCATGAAGTAATGTTCT
 CAGCT**TGA**TGACAAGGAACCTGTATAGTGATCCAGGGATGAACACCCCTGTGCGGTTTACT
 GTGGGAGACAGCCACCTTGAAGGGGAAGGAGATGGGAAGGCCCTTGCAGCTGAAAGTCC
 CACTGGCTGGCTCAGGCTGTCTTATTCGCTTGAAAATAGGCAAAAGTCTACTGTGGTAT
 TTGTAATAAACTCTATCTGCTGAAAGGGCTGCAGGCCATCCTGGGAGTAAAGGGCTGCCTT
 CCCATCTAATTTATTGTAAAGTCATATAGTCCATGTCTGTGATGTGAGCCAAGTGATATCCT
 GTAGTACACATTGTACTGAGTGGTTTTTCTGAATAAATCCATATTTTACCTATGA

FIGURE 322

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA92282

><subunit 1 of 1, 177 aa, 1 stop

><MW: 20452, pI: 8.00, NX(S/T): 2

MKLQCVSLWLLGTILILCSVDNHGLRRCLISTDMHHIEESFQEIKRAIQAKDTFPNVTILST
LETLQIIKPLDVCCVTKNLLAFYVDRVFKDHQEPNPKILRKISSIANSFLYMQKTLRQCQEQ
RQCHCRQEATNATRVIHNDYDQLEVHAAAIKSLGELDVFLAWINKNHEVMFSA

Signal sequence:

amino acids 1-18

N-glycosylation sites.

amino acids 56-60, 135-139

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 102-106

N-myristoylation site.

amino acids 24-30

Actinin-type actin-binding domain signature 1.

amino acids 159-169

FIGURE 323

CCCGTGCCAAGAGTGACGTAAGTACCGCCTATAGAGTCTATAGGCCCACTTGGCTTCGTTAG
 AACGCGGCTACAATTAATACATAACCTTATGTATCATACACATACGATTTAGGTGACACTAT
 AGAATAACATCCACTTTGCCTTTCTCTCCACAGGTGTCCACTCCCAGGTCCAAGTGCACCTC
 GGTTCTATCGATAATCTCAGCACCCAGCCACTCAGAGCAGGGCACGATGTTTGGGGGCCCGCCT
 CAGGCTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGCGTCCTCAGAGCCTATCCCA
 ATGCCTCCCCACTGCTCGGCTCCAGCTGGGGTGGCCTGATCCACCTGTACACAGCCACAGCC
 AGGAACAGCTACCACCTGCAGATCCACAAGAATGGCCATGTGGATGGCGCACCCCATCAGAC
 CATCTACAGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTGTGA
 TGAGCAGAAGATACCTCTGCATGGATTTTCTAGAGGCAACATTTTGGATCACACTATTTTCGAC
 CCGGAGAACTGCAGGTTCCAACACCAGACGCTGGAAAACGGGTACGACGTCTACCCTCTCC
 TCAGTATCACTTCCTGGTTCAGTCTGGGCCGGGCGAAGAGAGCCTTCCTGCCAGGCATGAACC
 CACCCCCGTACTCCAGTTTCTGTCCCGAGGAACGAGATCCCCCTAATTCACCTTCAACACC
 CCCATACCACGGCGGCACACCCGGAGCGCCGAGGACGACTCGGAGCGGGACCCCCGTAACGT
 GCTGAAGCCCCGGGCCCGGATGACCCCGCCCCGGCCTCCTGTTACAGGAGCTCCCGAGCG
 CCGAGGACAACAGCCCGATGGCCAGTGACCCATTAGGGGTGGTCAGGGGCGGTTCAGTGAAC
 ACGCACGCTGGGGGAACGGGCCCGGAAGGCTGCCGCCCTTCGCCAAGTTCATCTAGGGTCG
 CTGG

FIGURE 324

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA142238

><subunit 1 of 1, 251 aa, 1 stop

><MW: 27954, pI: 9.22, NX(S/T): 1

MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSWSGGLIHYLTATARNSYHLQIHKNGHVD
GAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIIFGSHYFDPENCRFQHQTLENGY
DVIHSPQYHFLVSLGRAKRAFLPGMNPPPYSQLSRRNEIPLIHFNTPIPRRHTRSAEDDSE
RDPLNLVKPRARMTFAPASCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTGPEGCRPFA
KFI

Important features of the protein:

Signal peptide:

amino acids 1-24

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 175-179

N-myristoylation site.

amino acids 33-39, 100-106, 225-231, 229-235

HBGF/FGF family proteins

amino acids 73-124

FIGURE 325

GGAAAAGGTACCCGCGAGAGACAGCCAGCAGTTCTGTGGAGCAGCGGTGGCCGGCTAGG**ATG**
 GGCTGTCTCTGGGGTCTGGCTCTGCCCTTTTCTTCTCTGCTGGGAGGTTGGGGTCTCTGG
 GAGCTCTGCAGGCCCCAGCACCCGCGAGAGCAGACTGCGATGACAACGGACGACACAGAAG
 TGCCCGCTATGACTCTAGCACCGGGCCAGCCGCTCTGGAACTCAAACGCTGAGCGCTGAG
 ACCTCTTCTAGGGCTCAACCCAGCCGGCCCCATTCAGAAGCAGAGACCAGGGGAGCCAA
 GAGAATTTCCCTGCAAGAGAGACCAGGAGTTTCAAAAAACATCTCCAACTTCATGGTGC
 TGATCGCCACCTCCGTGGAGACATCAGCCGCCAGTGCGACGCCCCGAGGGAGCTGGAATGACC
 ACAGTTCAGACCATCACAGGCAGTGATCCCGAGGAAGCCATCTTTGACACCCCTTTCACCGA
 TGACAGCTCTGAAGAGGCAAAGACACTACAATGGACATATTGACATTGGCTCACACCTCCA
 CAGAAGCTAAGGGCTGTCTCAGAGAGCAGTGCCCTCTCCGACGGCCCCCATCCAGTCATC
 ACCCCGTACAGGGCTCAGAGAGCAGCGCTCTTCCGACGGCCCCCATCCAGTCATCACCCC
 GTCACGGGCTCAGAGAGCAGCGCTCTTCCGACGGCCCCCATCCAGTCATCACCCGTCAT
 GGTCCCCGGGATCTGATGTCACTCTCTCTGCTGAAGCCCTGGTGACTGTGCACAAACATCGAG
 GTTATTAATTGCAGCATCACAGAAATAGAAACAACAACTTCAGCATCCCTGGGGCTCAGA
 CATAGATCTCATCCCCACGGAAGGGGTGAAGGCCCTCGTCCACCTCCGATCCACCAGCTCTGC
 CTGACTCCACTGAAGCAAAACACACATCACTGAGGTACAGCCTCTGCCGAGACCTGTCC
 ACAGCCGGCACCACAGAGTCAGCTGCACCTCATGCCACGGTTGGGACCCCACTCCCACTAA
 CAGCGCCACAGAAAGAGAAGTGACAGCACCCGGGGCCACGACCCTCAGTGAGACTCTGGTCA
 CAGTTAGCAGGAATCCCTTGAAGAACCTCAGCCCTCTCTGTTGAGACCAAGTTACGTC
 AAAGTCTCAGGAGCAGCTCCGGTCTCCATAGAGGCTGGGTGAGCTGGGCAAAACAACCTTC
 CTTTGTCTGGGAGCTCTGCTTCTCTACAGCCCTCGGAAGCCGGCTCAAGAAGTTACCCC
 CTTAGAGACACCGACCATGGACATCGCAACCAAGGGGCCCTTCCCCACAGCAGGGACCCCT
 CTTCTTCTGTCCCTCCGACTACAACCAACAGCAGCCGAGGGACGAACAGCACCTTAGCCAA
 GATCACAACTCAGCGAAGACCAGATGAAGCCCCAACAGCCACGCCCAGACTGCCCGGAC
 GAGGCCGACCACAGAC**TGA**GTGCAGGTGAAATGGAGGTTTCTCTCTCTGCGGCTGAGTG
 TGGCTTCCCCGGAAGACCTCACTGACCCAGAGTGGCAGAAAGGCTGATGCAGCAGCTCCAC
 CGGGAACCTCACGCCCCAGCGCTCACTTCCAGGTCTCCTTACTGCGTGTGAGAGAGGCTA
 ACGGACATCAGTGCAGCCAGGCATGTCCCGTATGCCAAAGAGGGTGTGCCCTAGCCTG
 GGCCCCACCGACAGACTGCAGCTGCGTTACTGTGCTGAGAGGTACCCAGAAAGGTTCCCATG
 AAGGGCAGCATGTCCAAGCCCTAACCCAGATGTGGCAACAGGACCTCGCTCACATCCAC
 CGGAGTGTATGTATGGGGAGGGGCTTCACTGTTCCAGAGGTGCTTGGACTCACCTTGG
 CACATGTTCTGTGTTTCAGTAAAGAGAGACCTGATACCCATCTGTGTGCTTCCATCTGCA
 TTAATTCACCTCAGTGTGGCCCCAAAAAAA

FIGURE 326

MGCLWGLALPLFFFCWEVGVSGSSAGPSTRRADTAMTTDDTEVPAMTLAPGHAALETQTLSEA
 ETSSRASTPAGPIPEAETRGAKRISPARETRSF TKTSPNFMVLIATSVETSAASGSPEGAGM
 TTVQITITGSDPEEAIFDTLCTDDSSSEAKTLM DILT LAHTSTEAKGLSSSESSASSDGPHPV
 ITPSRASESSASSDGPHPVITPSRASESSASSDGPHPVITPSWSPGSDVTL LAEALVTVTNI
 EVINCSITEIETTTSSIPGASDIDLIPTEGVKASSTSDPPALPDSTEAKPHITEVTASAETL
 STAGTTESAAPHATVGTPLPTNSATEREVTAPGATTLGALVTVSRNPLEETSALS SVETPSY
 VKVSGAAPVSI EAGSAVGKTTSFAGSSASSYSPSEAALKNFTPSETPTMDIATKGFPTSRD
 PLPSVPPTTTN SSRGTNSTLAKITTS AKTTMKPQQPRPRLPGRGRPQT

N-glycosylation sites:

amino acids 252-256, 445-449, 451-455

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 84-90

Casein kinase II phosphorylation sites.

amino acids 37-41, 108-112, 131-135, 133-137, 148-152, 165-169,
 246-250, 254-258, 256-260, 269-273, 283-287, 333-337, 335-339,
 404-408, 414-418, 431-435

N-myristoylation sites.

amino acids 2-8, 19-25, 117-123, 121-127, 232-238, 278-284, 314-
 320, 349-355, 386-392, 397-403, 449-455

ATP/GTP-binding site motif A (P-loop).

amino acids 385-393

FIGURE 327

GCGGAGCATCCGCTGCGGTCCTCGCCGAGACCCCGCGCGGATTGCGCGGTCTTCCCGCGG
 GCGCGACAGAGCTGTCTCGCACCTGGATGGCAGCAGGGGCGCGGGGTCTCTCGACGCCA
 GAGAGAAATCTCATCTCTGTGCAGCCTTCTTAAAGCAAACCTAAGACCAGAGGGAGGATTAT
 CCTTGACCTTTGAAGACCAAACCTAAACTGAAATTTAAATGTTCTTCGGGGGAGAGGGGAG
 CTTGACTTTACACTTTGGTAATAATTTGCTTCCCTGACACTAAGGCTGTCTGCTAGTCAGAATT
 GCCTCAAAAAGAGTCTAGAAGATGTTGTCAATTGACATCCAGTCATCTCTTTCTAAGGGAATC
 AGAGGCAATGAGCCCGTATATACTTCAACTCAAGAAGACTGCATTAATCTTGTCTGTTCAAC
 AAAAAACATATCAGGGGACAAAGCATGTAACCTTGATGATCTTCGACACTCGAAAAACAGCTA
 GACAACCCAACTGCTACCTATTTTTCTGTCCCAACGAGGAAGCCTGTCCATTGAAACCAGCA
 AAAGGACTTATGAGTTACAGGATAATTACAGATTTTCCATCTTTGACCAGAAATTTGCCAAG
 CCAAGAGTTACCCAGGAAGATTCTCTCTTACATGGCCAATTTTACAAAGCAGTCACCTCCCC
 TAGCCCATCATCACAGATTATTCAAAGCCACCGATATCTCATGGAGAGACACACTTTCT
 CAGAAGTTTGGATCCTCAGATCACCTGGAGAAACTATTTAAGATGGATGAAGCAAGTGCCCA
 GCTCCTTGCTTATAAGGAAAAAGGCCATTCTCAGAGTTCAACAATTTTCTCTGATCAAGAAA
 TAGCTCATCTGCTGCGCTGAAAATGTGAGTGCGCTCCAGCTACGGTGGCAGTTGCTTCTCCA
 CATACCACCTCGGCTACTCCAAAGCCCGCCACCTTCTACCCACCAATGCTTCAGTGACACC
 TTCTGGGACTTCCAGCCACAGCTGGCCACCACAGCTCCACCTGTAACCACTGTCACTTCTC
 AGCCTCCACGACCCCTCATTTCTACAGTTTTTACAGGGGCTCGGCTACACTCCAAAGCAATG
 GCTACAACAGCAGTTCTGACTACCACCTTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGA
 AACCATACCGTTTTACAGAAATCTCCAACTTAACTTTGAACACAGGGAATGTGTATAACCTTA
 CTGCACCTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAAACTGCTTCTCTGGGAAGGT
 AGGGAGGCCAGTCCAGGCAGTTCTCCAGGGGCAGTGTTCCAGAAAATCAGTACGGCCTTCC
 ATTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCTGTTCCCTGGTGATAGGCC
 TCGTCTCTCTGGGTAGAATCCTTTTCGGAATCACTCCGCAGGAAACGTTACTCAAGACTGGAT
 TATTTGATCAATGGGATCTATGTGGACATCTAAGGATGGAACCTCGGTGTCTCTTAATTCATT
 TAGTAACCCAGAAGCCCAATGCAATGAGTTTCTGCTGACTTGTAGTCTTAGCAGGAGGTTG
 TATTTTGAAGACAGGAAAATGCCCCCTTCTGCTTTCTCTTTTTTTTTTTGGAGACAGAGCTTT
 GCTCTGTTGCCAGGCTGGAGTGCACTAGCAGCATCTCGGCTCTCACCGCACCTCCGCTCTC
 CTGGGTTCAAGCGATTCTCTCGCCTCAGCCTCCTAAGTATCTGGGATTACAGGCATGTGCCA
 CCACACCTGGGTGATTTTTGTATTTTAGTAGAGACGGGGTTTACCATTGTTGGTCAGGCTG
 GTCTCAAACCTCTGACCTAGTGATCCACCCTCTCGGCTCCCAAAGTGTCTGGGATTACAGG
 CATGACCCACCAAGCTGGCCCCCTTCTGTTTTATGTTTGGTTTTTGGAGGAAGTAAGTGT
 GGAACCAAATTAGGTAATTTTGGGTAATCTGTCTCTTAAATATTAGCTAAGAAACAAAGCTCT
 ATGTAAGTAATAAAGTATAAATTGCCATATAAATTTCAAATTCACCTGGCTTTTATGCAAA
 GAAACAGTTTAGGACATCTAGGTTCCAATTCATTCACTTCTGGTCCAGATAAAATCAAC
 TGTTTATATCAATTTCTAATGGATTGCTTTCTTTTATATGATTCCTTTAAACTTATT
 CCAGATGTAGTTCTCTCCAATTAATATTTGAATAAATCTTTTGTACTCAA

FIGURE 328

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45410
><subunit 1 of 1, 431 aa, 1 stop
><MW: 46810, pI: 6.45, NX(S/T): 6
MFFGGEGSLTYTLVVIICFLTTLRLSASQNCCLKSLEDVVIDIQSSLSKGIRGNEPVYTSTQED
CINSCCSTKNISGDKACNLMI F DTRKTRARQPNCYLFFCPNEEACPLKPAKGLMSYRIITDFP
SLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSDHLEKLF
KMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHSTTSATPKPATLL
PTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATTAVLTTFQAP
TDSKGSLETIPFTEISNLTNLNTGNVYNPTALSMSNVESSTMNKITASWEGREASPGSSSQGSV
PENQYGLPFEKWLLIGSLFLFGVLFLVIGLVLLGRILSESLRRKRYSRLDYLINGIYVDI
```

Signal sequence.

amino acids 1-25

Transmembrane domain.

amino acids 384-405

N-glycosylation sites.

amino acids 72-76, 222-226, 251-255, 327-331, 352-356

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 415-419

Tyrosine kinase phosphorylation site.

amino acids 50-57

N-myristoylation sites.

amino acids 4-10, 48-54, 315-321

FIGURE 329

CTCCACGGTGTCCAGCGCCAGAAATGCGGCTTCTGGTCTGCTATGGGGTTGCTGCTGCT
 CCCAGGTTATGAAGCCCTGGAGGGCCAGAGGAAATCAGCGGGTTCAAGGGGACACTGTGT
 CCCTGCAGTGCACCTACAGGGAAGAGCTGAGGGACCACCGGAAGTACTGGTGCAGGAAGGGT
 GGGATCCTCTTCTCTCGTCTCTGGCACCATTCTATGCAGAAGAAGAGGCCAGGAGACAAT
 GAAGGGCAGGGTGTCCATCCGTGACAGCCGCCAGGAGCTCTCGTCTATTGTGACCCCTGTGGA
 ACCTCACCTTGAAGACGCTGGGGAGTACTGGTGTGGGGTCGAAAAACGGGGGCCCGATGAG
 TCTTTACTGATCTCTCTGTTCGTCTTCCAGGACCCTGCTGTCTCTCCCTCCCTTCTCCAC
 CTTCAGCCTCTGGCTACAACACGCTTGCAGCCCAAGCAAAAGCTCAGCAAAACCAGCCCC
 CAGGATTGACTTCTCTGGGCTCTACCCGGCAGCCACCACAGCCAAAGCAGGGGAAGACAGGG
 GCTGAGGCCCCCTCCATTGCCAGGGACTTCCAGTACGGGCACGAAGGACTTCTCAGTACAC
 AGGAACCTCTCTCACCAGCGACCTCTCTCTCTGCAAGGAGCTCCCGCCCCCCATCTCAGC
 TGGACTCCACCTCAGCAGAGGACACCACTCCAGCTCTCAGAGTGGCAGCTCTAAGGCCAGG
 GTGTCCATCCCGATGGTCCGCATACTGGCCCCAGTCTGGTGTCTGCTGAGCCTTCTGTGAGC
 CGCAGGCTGATCGCCTTCTGAGCCACCTGCTCCTGTGGAGAAAGGAAGCTCAACAGGCCA
 CGGAGACACAGAGGAACGAGAAGTTCTGGCTCTCAGCTTGACTCGGAGGAAAGGAAGCC
 CTTTCCAGGCCCCCTGAGGGGGACGTGATCTGATGCCTCCCTCCACATCTGAGGAGGA
 GCTGGGCTTCTCGAAGTTTGTCTCAGCGTAGGGCAGGAGGCCCTCTTGCCACAGCCAGCAGT
 GAAGCAGTATGGCTGGCTGGATGCAGCACCAGTTCCGAAAGCTTCCCTACCTCAGCCTCAGAG
 TCCAGCTGCCCGGACTCGAGGGCTCTCCCCACCCTCCCCAGGCTCTCTCTTGATATGTTCCA
 GCTGACCTAGAAGCGTTTGTGAGCCCTGGAGCCAGAGCGGTGGCCTTGCTCTTCCGGCTG
 GAGACTGGGACATCCCTGATAGGTTACATCCCTGGGCAGAGTACCAGGCTGCTGACCCCTCA
 GCAGGGCCAGACAAGGCTCAGTGGATCTGGTCTGAGTTTCAATCTGCCAGGAACCTCTGGGC
 CTCATGCCCAGTGTGCGGCCCTGCCTTCTCCCACTCCAGACCCACCTTGCTTCTCCCTCCC
 TGGCGTCTCTCAGACTTAGTCCACGGTCTCTGCTCAGCTGGTGTGATGAAGAGGAGCATGCT
 GGGGTGAGACTGGGATTCTGGCTTCTCTTTGAACCACCTGCATCCAGCCCTTCAGGAAGCCT
 GTGAAAAACGTGATTCTCTGGCCCCACCAAGACCCACCAAAACCATCTCTGGGCTTGGTGCAG
 GACTCTGAATTCTAACAATGCCAGTGACTGTGCACTTGAGTTTGAAGGCCAGTGGGCCCTG
 ATGAACGCTCAACCCCTTCAGCTTAGAGTCTGCATTGGGCTGTGACGTCTCCACCTGCC
 CAATAGATCTGCTCTGTCTGCGACACCAGATCCACGTGGGGACTCCCCTGAGGCTGCTAAG
 TCCAGGCTTGGTCAGGTCAAGTGCACATTGCAGGATAAGCCAGGACCGGCACAGAAGTGG
 TTGCTTTTNCATTTGCCCTCCCTGGNCCATGCCTTCTGCTTTGGAAAAAATGATGAAGA
 AAACCTTGGTCTCTCTGTCTGAAAGGGTTACTTGCCTATGGGTTCTGGTGGCTAGAGA
 GAAAAGTAGAAAACAGAGTGACGTAGGTGTCTAACACAGAGGAGAGTAGGAACAGGGCGG
 ATACCTGAAGGTGACTCCGAGTCCAGCCCCCTGGAGAAGGGGTCCGGGGTGGTGTAAAGTA
 GCACAACACTATATTTTTTTCTTTTCCATTATATTGTTTTTAAAGACAGATCTCGTGCT
 GCTGCCACAGCTGGAGTGGCAGTGCCACGATCTGCAACTCCGCCTCTCGGTTTCAAGTGATT
 CTTCTGCCTCAGCCTCCGAGTAGCTGGGATTACAGGCACGCACCACCACCTGGCTAATT
 TTTGTACTTTTAGTAGAGATGGGGTTTACCATTGTGGCCAGGCTGGTCTGAACTCCTGAC
 CTCAATGAGCCTCTGCTTCACTCTCCAAATGTCGGGATTACAGCACTGAGCCACTGTG
 TCTGGCCCTATTTCTTTTAAAGAGTAAATTAAGAGTTGTTCAAGTATGCAAACTTGGAAAG
 ATGGAGGAGAAAAAGAAAGAAAAAAGTACCCATAGTCTCACCAGAGACTATCAT
 TATTTCTGTTTGTGTACTTCTTCCACTCTTTCTTCTTACATAATTTCGGGTGTTCTT
 TTTACAGAGCAATATCTGTATATACAACTTTGTATCCTGCCTTTTCCACCTTATCGTTC
 ATCACTTTATTCAGCACTTCTCTGTGTTTTACAGACCTTTTATAAATAAATGTTATCA
 GCTGCATAAAAAAAAAAAAAA

